

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:41:38 ; Search time 33 Seconds

(without alignments)
26.218 Million cell updates/sec

Title: US-09-692-401-4

Perfect score: 46

Sequence: 1 VRIGHLYIL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 789

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	37.0	4	2 I38888	COI intron 16 prot
2	17	37.0	9	2 S07205	litorin 2-Glu - Au
3	17	37.0	9	2 S07204	litorin I - Austr
4	17	37.0	9	2 S39437	D-amino-acid oxida
5	15	32.6	4	2 PL0140	carbon-monoxide de
6	15	32.6	7	2 A28709	phosphonoacetaldeh
7	15	32.6	9	2 PT0238	Ig heavy chain CRD
8	14	30.4	3	3 GKHU	growth-modulating
9	14	30.4	6	2 A61419	sarcosine dehydrog
10	14	30.4	6	2 B56979	collagen alpha 1(I
11	14	30.4	7	1 NYF07	hypothalamic hepta
12	14	30.4	7	2 S42407	granulysin S synth
13	14	30.4	8	2 A61467	penalbumin - Adeli
14	14	30.4	9	2 S07241	litorin - Rohde's
15	13	28.3	4	2 PT0721	T-cell receptor be
16	13	28.3	7	2 A60139	fatty-acid synthas
17	13	28.3	7	2 PQ0663	membrane protein -
18	13	28.3	7	2 A23269	sex pheromone cAM3
19	13	28.3	7	4 I56695	hypothetical I2 pr
20	13	28.3	9	2 S78420	ribosomal protein
21	12	26.1	4	2 A48360	gamma subunit of p
22	12	26.1	6	2 A60986	N-formyl oligopept
23	12	26.1	7	2 S45311	microcin C7 - Esch
24	12	26.1	8	2 B45800	serum albumin - do
25	12	26.1	8	2 PC4373	telomeric and tetr
26	12	26.1	9	2 S13636	coat protein beta
27	12	26.1	9	2 JN0026	sperm-activating p
28	12	26.1	9	2 G58502	kidney and bladder
29	12	26.1	9	2 B39841	dextranucrase (EC

30 11 23.9 5 2 PQ0009 angiotensin-conver
31 11 23.9 5 3 J08070 phytosulfokine alp
32 11 23.9 7 2 S71867 glutathione transf
33 11 23.9 7 2 S08606 hypothetical prote
34 11 23.9 7 2 A11483 aspartate transami
35 11 23.9 7 2 S38797 serine/threonine-s
36 11 23.9 7 2 S33567 tubulin beta-3 cha
37 11 23.9 8 2 S66646 cardiocaceleratory
38 11 23.9 8 2 PH1618 Ig H chain V-D-J r
39 11 23.9 8 2 PN0043 phosphatidylethano
40 11 23.9 8 2 PC4372 telomeric and tetr
41 11 23.9 8 2 T13818 cytochrome oxidase
42 11 23.9 9 2 A91466 oxytocin - hippopo
43 11 23.9 9 2 A92774 oxytocin - spotted
44 11 23.9 9 2 A93147 oxytocin - finback
45 11 23.9 9 2 A93408 oxytocin - Austral

ALIGNMENTS

RESULT 1

I38888 COI intron 16 protein - Podospora anserina mitochondrion

C:Species: mitochondrion Podospora anserina

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999

C:Accession: I38888

R:Cummings, D.J.; Michel, F.; McNally, K.L.

A:Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I

A:Reference number: A48327; MUID:90124722; PMID:2558809

A:Accession: I38888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4 <CUM>

C:Cross-references: GB:X55026; GB:M30937; GB:M61734

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC3

C:Keywords: mitochondrion

Query Match 37.0%; Score 17; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIGH 5

DB 1 QLGH 4

RESULT 2

S07205 litorin 2-Glu - Australian tree frog (Litoria aurea)

C:Species: Litoria aurea

C>Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C:Accession: S07205

R:Anastasi, A.; Montecucchi, P.; Angelucci, F.; Erspamer, V.; Endeane, R.

Experientia 33, 1289, 1977

A:Title: Glu(OMe)(2)-litorin, the second bombesin-like peptide occurring in methanol

A:Reference number: S07205; MUID:78003546; PMID:908397

A:Accession: S07205

A:Molecule type: protein

A:Residues: 1-9 <ANA>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.0%; Score 17; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGH 5

Db 5 VGH 7
:||

RESULT 3
S07204

litorin I - Australian tree frog (Litoria aurea)
C;Species: Litoria aurea
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07204

R;Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 510-511, 1975

A;Title: Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide from
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Met) #status experimental

A;Accession: S07204

A;Molecule type: protein

A;Residues: 1-9 <ANA>

C;Superfamily: gastrin-releasing peptide

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.0%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGH 5

:||

Db 5 VGH 7

RESULT 4
S39437

D-amino-acid oxidase (EC 1.4.3.3) - Trigonopsis variabilis (fragment)

C;Species: Trigonopsis variabilis

C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1997 #text_change 07-May-1999

C;Accession: S39437

R;Schraeder, T.; Andreesen, J.R.

Eur. J. Biochem. 216, 735-744, 1993

A;Title: Evidence for the functional importance of Cys298 in D-amino acid oxidase from T
A;Reference number: S39437; MUID:94094869; PMID:7903639

A;Accession: S39437

A;Molecule type: protein

A;Residues: 1-9 <SCH>

A;Experimental source: CBS 4095

C;Function:

A;Description: oxidoreductase; catalyzes the oxidation of D-amino acids to their corres

A;Note: reoxidation of the enzyme by molecular oxygen is accompanied by the release of H

C;Keywords: FAD; oxidoreductase

Query Match 37.0%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGH 5

:||

Db 2 VGH 4

RESULT 5
PL0140

Carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena

C;Species: Pseudomonas carboxydohydrogena

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993

C;Accession: PL0140

R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.

Arch. Microbiol. 152, 335-341, 1989

A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotro

A;Reference number: PL0138; MUID:90055678; PMID:2818128

A;Accession: PL0140

A;Molecule type: protein

A;Residues: 1-4 <KRA>

C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, md

C;Keywords: oxidoreductase

Query Match 32.6%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGH 5

:||

Db 1 MGH 3

RESULT 6
A28709

phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)

C;Species: Bacillus cereus

C;Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993

C;Accession: A28709

R;Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.

Biochemistry 27, 2229-2234, 1988

A;Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Eviden
idue.

A;Reference number: A28709; MUID:88241058; PMID:3132206

A;Accession: A28709

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <OLS>

Query Match 32.6%; Score 15; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VRIGHL 6

:|| |:

Db 1 LKIDHV 6

RESULT 7
PT0238

Ig heavy chain CDR3 region (clone 2-94B) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0238

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0238

A;Molecule type: DNA

A;Residues: 1-9 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 32.6%; Score 15; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 IGHLY 7

:||

Db 4 VDHSY 8

RESULT 8
GKHU

growth-modulating peptide - human

C;Species: Homo sapiens (man)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A01421

R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.

Experientia 33, 324-325, 1977

A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.

A;Reference number: A01421; MUID:77162369; PMID:858356

A;Accession: A01421

A;Molecule type: protein

A;Residues: 1-3 <SCH>
A;Note: this serum tripeptide is found to stimulate growth of some cell types and to inh
C;Superfamily: unassigned animal peptides

Query Match 30.4%; Score 14; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GH 5
||
Db 1 GH 2

RESULT 9
A61419
sarcosine dehydrogenase (EC 1.5.99.1) - Pseudomonas sp. (strain WRF) (fragment)
C;Species: Pseudomonas sp.
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C;Accession: A61419
R;Pinto, J.T.; Frisell, W.R.
Arch. Biochem. Biophys. 169, 483-491, 1975
A;Title: Characterization of the peptide-bound flavin of a bacterial sarcosine dehydroge
A;Reference number: A61419; MUID:76038634; PMID:241294
A;Accession: A61419
A;Molecule type: protein
A;Residues: 1-6 <PIN>
C;Keywords: PAD; flavoprotein; oxidoreductase; phosphoprotein
F;6/Modified site: 3'-PAD-histidine (His) #status experimental

Query Match 30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GH 5
||
Db 5 GH 6

RESULT 10
B56979
collagen alpha 1(II) chain - bovine (fragment)
N;Alternate names: collagen alpha 3(XI) chain
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C;Accession: B56979
R;Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A;Title: Structural analysis of cross-linking domains in cartilage type XI collagen. Ins
A;Reference number: A56979; MUID:95370194; PMID:7642541
A;Accession: B56979
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-6 <WUA>
A;Note: the residue designated "x" is modified Lysine in collagen 1(II) some cross-linke

Query Match 30.4%; Score 14; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GH 5
||
Db 4 GH 5

RESULT 11
NPG7
hypothalamic heptapeptide - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 23-Aug-1996
C;Accession: A01417
R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong,
Horm. Metab. Res. 13, 228-232, 1981
A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-releas

A;Reference number: A01417; MUID:81213980; PMID:6263778
A;Accession: A01417
A;Molecule type: protein
A;Residues: 1-7 <CHA>
C;Superfamily: hypothalamic heptapeptide
C;Keywords: hypothalamus

Query Match 30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 IGHLY 7
| | |
Db 2 IYHSY 6

RESULT 12
S42407
gramicidin S synthetase component II - Bacillus brevis (fragment)
C;Species: Bacillus brevis
C;Date: 20-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C;Accession: S42407
R;Stein, T.; Vater, J.; Kruff, V.; Wittmann-Liebold, B.; Franke, P.; Panico, M.; Mc D
FEBS Lett. 340, 39-44, 1994
A;Title: Detection of 4'-phosphopantetheine at the thioester binding site for L-valin
A;Reference number: S42407; MUID:94164305; PMID:8119405
A;Accession: S42407
A;Molecule type: protein
A;Residues: 1-7 <STE>

Query Match 30.4%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GH 5
||
Db 3 GH 4

RESULT 13
A61467
penalbumin - Adelie penguin (fragment)
C;Species: Pygoscelis adeliae (Adelie penguin)
C;Date: 07-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 04-Nov-1994
C;Accession: A61467
R;Osuga, D.F.; Aminlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.E.
J. Protein Chem. 2, 43-62, 1983
A;Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparis
A;Reference number: A61467
A;Accession: A61467
A;Molecule type: protein
A;Residues: 1-8 <OSU>
C;Comment: Penalbumin is a major protein component of egg whites from penguins but no
C;Keywords: egg white; glycoprotein

Query Match 30.4%; Score 14; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GHLY 7
| | |
Db 1 GSIY 4

RESULT 14
S07241
litorin - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07241
R;Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspame
FEBS Lett. 182, 53-56, 1985
A;Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.

A:Reference number: S07241; MUID:85127560; PMID:3838283

A:Accession: S07241

A:Molecule type: protein

A:Residues: 1-9 <BAR>

C:Superfamily: gastrin-releasing peptide

C:Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

30.4%; Score 14; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GH 5

Db 6 GH 7

RESULT 15

PT0721

T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0721

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0721

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-4 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match

28.3%; Score 13; DB 2; Length 4;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIG 4

Db 2 RLG 4

Search completed: December 19, 2002, 16:45:39

Job time : 34 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:40:38 : Search time 10 seconds
(without alignments)
37.329 Million cell updates/sec

Title: US-09-692-401-4
Perfect score: 46
Sequence: 1 VRIGHLYIL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 231

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	17	37.0	9	LITO_LITAU	P08945 litoria aur
2	16	34.8	9	NEUX_HUMAN	P04277 homo sapien
3	16	34.8	9	NSK1_SARBU	P41492 sarcophaga
4	15	32.6	4	DCML_PSECH	P19916 pseudomonas
5	14	30.4	3	GRWM_HUMAN	P01157 homo sapien
6	14	30.4	7	FAR2_ASCSU	P31890 ascaris suu
7	14	30.4	7	HY7_PIG	P01153 sus scrofa
8	14	30.4	9	LITR_PHYRO	P08946 phyllomedus
9	13	28.3	7	CIA_ENTFA	P11932 enterococu
10	13	28.3	7	GFRP_MOUSE	P99025 mus musculu
11	13	28.3	9	PGLR_DIAAB	P81179 diaprepes a
12	12	26.1	8	ANG2_BOTJA	Q10582 bochrops ja
13	12	26.1	9	MOSH_CLYJA	P19852 clypeaster
14	12	26.1	9	RE42_LITRU	P82075 litoria rub
15	12	26.1	9	RS10_SERMA	O68936 serratia ma
16	11	23.9	5	FARP_ARTTR	P41853 artiposthi
17	11	23.9	5	PSK_DAUCA	P58261 daucus caro
18	11	23.9	7	UN06_PINPS	P81675 pinus pinas
19	11	23.9	8	ALL6_CYDPO	P82157 cydia pomon
20	11	23.9	9	ISOT_CYPCA	P42993 cyprinus ca
21	11	23.9	9	NEUT_CAVPO	P34966 cavia porce
22	11	23.9	9	OXYA_SCYCA	P42996 scyllorhinu
23	11	23.9	9	OXYA_SQUAC	P42999 squalus acu
24	11	23.9	9	OXYT_BUFRE	P42995 bufo regula
25	11	23.9	9	OXYT_CYPCA	P23879 cyprinus ca
26	11	23.9	9	OXYT_RABIT	P32878 cryctolagus
27	11	23.9	9	OXYT_RAJCL	P42994 raja clavat
28	11	23.9	9	OXYV_SQUAC	P43000 squalus acu
29	10	21.7	5	TPIS_CANFA	P54714 canis famil
30	10	21.7	5	UF01_MOUSE	P38639 mus musculu
31	10	21.7	6	FARP_MONEX	P41966 moniezia ex
32	10	21.7	7	FAR5_HIRME	P42564 hirudo medi
33	10	21.7	8	ACI_THUAL	P18691 thunnus alb

34	10	21.7	8	1	UF06_MOUSE	P38644 mus musculu
35	10	21.7	9	1	BUK_CLOPA	P81337 clostridium
36	10	21.7	9	1	IPYR_RHOVI	P82992 rhodopsedo
37	10	21.7	9	1	MOSF_CLYJA	P19853 clypeaster
38	10	21.7	9	1	OXYT_OCTVU	P80027 octopus vul
39	10	21.7	9	1	ULAD_HUMAN	P31929 homo sapien
40	10	21.7	9	1	XYLA_STRSQ	P19149 streptomyce
41	9	19.6	4	1	EOSI_HUMAN	P02731 homo sapien
42	9	19.6	4	1	FAR3_HIRME	P42562 hirudo medi
43	9	19.6	4	1	FYRI_ATEFL	P58706 anthopleura
44	9	19.6	5	1	BIOB_CITFR	P12997 citrobacter
45	9	19.6	5	1	PRCT_PERAM	P01373 periplaneta

ALIGNMENTS

RESULT 1

LITO_LITAU
ID LITO_LITAU STANDARD; PRT; 9 AA.
AC P08945;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Litorin.
OS Litoria aurea (Green and golden bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=8371;
RN [1]
RP SEQUENCE.
RX MEDLINE=75187011; PubMed=1140241;
RA Anastasi A., Erspamer V., Endean R.;
RT "Aminoacid composition and sequence of litorin, a bombesin-like
RT nonapeptide from the skin of the Australian leptodactylid frog
RT Litoria aurea.";
RL Experimentia 31:510-511(1975).
RN [2]
RP SEQUENCE (METHYLATED VARIANT).
RX MEDLINE=78003546; PubMed=908397;
RA Anastasi A., Montecucchi P.C., Angelucci F., Erspamer V., Endean R.;
RT "Glu(OMe)-litorin, the second bombesin-like peptide occurring in
RT methanol extracts of the skin of the Australian frog Litoria aurea.";
RL Experimentia 33:1289-1289(1977).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR: S07204; S07204.
DR PIR: S07205; S07205.
DR InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation; Methylation.
FT MOD_RES 1 2 METHYLATION (IN A VARIANT).
FT MOD_RES 2 9 AMIDATION.
SQ SEQUENCE 9 AA; 1103 MW; D7CCCEIE862CDC366 CRC64;

Query Match 37.0%; Score 17; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.le+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGH 5
:|:
Db 5 VGH 7

RESULT 2

NEUX_HUMAN
ID NEUX_HUMAN STANDARD; PRT; 9 AA.
AC P04277;
DT 20-MAR-1987 (Rel. 04, Created)

DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurotensin-related peptide (NRP) (Kin tensin).
 OS Homo sapiens (Human),
 OS Bos taurus (Bovine), and
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606, 9913, 9986;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human;
 RX MEDLINE=86242180; PubMed=3087352;
 RA Moqard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,
 RA Shively J.E., Walsh J.H.;
 RT "The amino acid sequence of kin tensin, a novel peptide isolated from
 RT pepsin-treated human plasma: homology with human serum albumin,
 RT neurotensin and angiotensin.";
 RL Biochem. Biophys. Res. Commun. 136:983-988(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Human, Bovine, and Rabbit;
 RX MEDLINE=87194805; PubMed=2437111;
 RA Carraway R.E., Mitra S.P., Cochrane D.E.;
 RT "Structure of a biologically active neurotensin-related peptide
 RT obtained from pepsin-treated albumin(s).";
 RL J. Biol. Chem. 262:5968-5973(1987).
 CC -1- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND
 CC BLOOD FLOW (POTENTIAL).
 DR PIR; A03239; ABHUSK.
 KW Hormone.
 DR PIR; A26693; A26693.
 SQ SEQUENCE 9 AA; 1172 MW; C804DB4761F4140D CRC64;

 Query Match 34.8%; Score 16; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 5 HLYIL 9
 | | |
 Db 5 HPYFL 9

 RESULT 3
 NSKL_SARBU STANDARD; PRT; 9 AA.
 AC P41492;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 01-FEB-1996 (Rel. 33, Last annotation update)
 DE Neosulfakinin-I (NEB-SK-I).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Oestroidea; Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RX MEDLINE=93083101; PubMed=1360367;
 RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
 RT "Isolation and primary structure of two sulfakinin-like peptides from
 RT the fleshfly, Neobellieria bullata.";
 RL Comp. Biochem. Physiol. 103C:135-142(1992).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; 1.
 KW Neuropeptide; Amidation; Sulfation.
 FT MOD_RES 4 4
 FT MOD_RES 9 9
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1187 MW; 8B0A0691E86B5AAA CRC64;

Query Match 34.8%; Score 16; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 4 GHL 6
 | |
 Db 5 GHM 7

 RESULT 4
 DCML_PSECH STANDARD; PRT; 4 AA.
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
 DE dehydrogenase subunit L) (CO-DH L) (Fragment).
 GN CUTL.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydohydrogenic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: Molybdenum (molybdopterin).
 CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; PLO140; PLO140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4 4
 SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

 Query Match 32.6%; Score 15; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 3 IGH 5
 : | |
 Db 1 MGH 3

 RESULT 5
 GRWM_HUMAN STANDARD; PRT; 3 AA.
 AC P01157;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Growth-modulating peptide.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77162369; PubMed=858356;
 RA Schlesinger D.H., Pickart L., Thaler M.M.;
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
 RL Experientia 33:324-325(1977).
 CC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
 CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
 CC PIR; A01421; GKHU.
 SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

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Query Match      30.4%; Score 14; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GH 5
   1 1
Db 1 GH 2

RESULT 6
FAR2_ASCSU
ID FAR2_ASCSU STANDARD; PRT; 7 AA.
AC P31890;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF2.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253, 6233;
RN [1]
RP SEQUENCE.
RC SPECIES=A.suum;
RX MEDLINE=93324431; PubMed=8332542;
RA Cowden C., Stretton A.O.W.;
RT "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
RL Peptides 14:423-430(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=P.redivivus;
RX MEDLINE=95060998; PubMed=7970891;
RA Maule A.G., Shaw C., Bowman J.W.;
RT "The FMRamide-like neuropeptide AF2 (Ascaris suum) is present in the
free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";
RL Parasitology 109:351-356(1994).
CC -1- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.
CC -1- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION
SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match      30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 HLXI 8
   1 1
Db 2 HEYL 5

RESULT 7
HV7_PIG
ID HV7_PIG STANDARD; PRT; 7 AA.
AC P01153;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Safran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
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RT "Isolation, structure and synthesis of a heptapeptide with in vitro
ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. 13:228-232(1981).
DR PIR; A01417; NYPG7.
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match      30.4%; Score 14; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 IGHLY 7
   1 1
Db 2 IVHSY 6

RESULT 8
LITR_PHYRO
ID LITR_PHYRO STANDARD; PRT; 9 AA.
AC P08946;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rhodei-litorin.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RX MEDLINE=85127560; PubMed=3838283;
RA Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P.,
RA Erspamer V.;
RT "Rhodei-litorin: a new peptide from the skin of Phyllomedusa rohdei.";
RL FEBS Lett. 182:53-56(1985).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; S07241; S07241.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1090 MW; 4ECCCE1E861ADC377 CRC64;

Query Match      30.4%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GH 5
   1 1
Db 6 GH 7

RESULT 9
CIA_ENTFA
ID CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
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RT CAM373.; 206:69-72(1986).
CC -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
CC HARBORING PAM373.
CC -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
CC -!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR; A25269; A25269.
KW Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 YLIL 9
DB 2 IFIL 5

RESULT 10
GFRP_MOUSE
ID GFRP_MOUSE STANDARD; PRT; 7 AA.
AC P99025;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN GCHFR OR GFRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA Cowthorne M.;
RA Submitted (AUG-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: MEDIATES TETRAHYDROBIPTERIN INHIBITION OF GTP
CC CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
CC (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
DR SWISS-2DPAGE; P99025; MOUSE.
FT INIT_MET 0
FT NON_TER 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 YIL 9
DB 2 YLL 4

RESULT 11
PGLR_DIAAB
ID PGLR_DIAAB STANDARD; PRT; 9 AA.
AC P81179;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).
OS Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Phytophaga; Curculionidae; Entiminae; Entimini;
OX Diaprepes.
OX NCBI_TaxID=13040;
RN [1]

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RP SEQUENCE.
RC TISSUE=Larval gut;
RA Doostdar H., McCollum T.G., Mayer R.T.;
RT "Purification and characterization of an endo-polygalacturonase from
RT the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes
RT abbreviatus L.) larvae.";
RC Comp. Biochem. Physiol. 118B:861-867(1997).
CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -!- INDUCTION: INHIBITED BY CITRUS PCIP.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 9.4, ITS MW IS: 44.5 kDa.
CC -!- SIMILARITY: WEAK, TO OTHER POLYGALACTURONASES.
KW Hydrolase; Glycosidase; Cell wall.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1041 MW; 1F49087042DB41BB CRC64;

Query Match 28.3%; Score 13; DB 1; Length 9;
Best Local Similarity 20.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 HLXIL 9
DB 2 YTYVI 6

RESULT 12
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OX Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 26.1%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LYI 8
DB 3 VII 5

RESULT 13
MOSH_CLYJA
ID MOSH_CLYJA STANDARD; PRT; 9 AA.
AC P19852;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE [His-6]-mosact.
OX Glypeaster japonicus (Sand dollar).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;

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OC Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
OC Clypeasteridae; Clypeaster.
OX NCBI_TaxID=7644;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg jelly;
RA Suzuki N., Kurita M., Yoshino K.I., Kajiuira H., Nomura K.,
RA Yanaguchi M.;
RT "Purification and structure of mosact and its derivatives from the
RT egg jelly of the sea urchin Clypeaster japonicus.";
RL Zool. Sci. 4:649-656(1987).
CC -!- FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.
DR PIR; JN0026; JN0026.
SQ SEQUENCE 9 AA; 914 MW; 93245721EDC5BAB5 CRC64;

Query Match 26.1%; Score 12; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HL 6
   ||
Db 6 HL 7

RESULT 14
RE42_LITRU STANDARD; PRT; 9 AA.
AC P82075; P82093;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Rubellidin 4.2/4.3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the australin red tree frog
RT 'Litoria rubella', the skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
RN [2]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
CC -!- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
CC terminal amidation.
CC -!- MASS SPECTROMETRY: MW=883; METHOD=FA-B.
KW Amphibian skin; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 884 MW; 2C2D77205AA72728 CRC64;

Query Match 26.1%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GHLVIL 9
   | | | |
Db 2 GLLDIL 7

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RESULT 15
RS10_SERMA STANDARD; PRT; 9 AA.
ID RS10_SERMA
AC O68936;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10 (Fragment).
GN RPSJ.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RA Noorani S.M., Lindahl L., Zengel J.M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF058451; AAC14294.1; -
CC DR InterPro; IPR001848; Ribosomal_S10.
CC DR PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
CC KW Ribosomal protein.
CC FT NON_TER 9 9
CC SQ SEQUENCE 9 AA; 1214 MW; DE3944004416D456 CRC64;

Query Match 26.1%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRI 3
   : | |
Db 6 IRI 8

Search completed: December 19, 2002, 16:44:58
Job time : 11 secs

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OM protein - protein search, using sw model
Run on: December 19, 2002, 16:39:43 ; Search time 56 Seconds
(without alignments)
33.115 Million cell updates/sec

Title: US-09-692-401-4
Perfect score: 46
Sequence: 1 VRIGHLYIL 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 686
Minimum DB seq length: 0
Maximum DB seq length: 9
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_nhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvrius.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	52.2	7	10	P82445
2	19	41.3	9	4	Q14277
3	17	37.0	7	12	Q9YQ10
4	16	34.8	8	2	Q93SP2
5	15	32.6	8	8	Q9XNP8
6	14	30.4	9	2	Q47410
7	14	30.4	9	5	Q9VW82
8	14	30.4	9	11	O08979
9	13	28.3	7	11	Q63480
10	13	28.3	8	4	Q9UMC7
11	13	28.3	8	8	Q34909
12	13	28.3	8	8	O8WGC7
13	13	28.3	8	12	Q83332
14	13	28.3	9	2	P83222
15	13	28.3	9	4	Q9UQA3
16	12	26.1	7	2	Q47505

17	12	26.1	7	8	O99182
18	12	26.1	8	2	Q9AGP4
19	12	26.1	8	5	Q9VRD2
20	12	26.1	8	6	Q9XSY1
21	12	26.1	9	2	Q9R7E8
22	12	26.1	9	4	Q99887
23	12	26.1	9	4	Q9UM87
24	12	26.1	9	11	Q99MG3
25	12	26.1	9	11	Q61723
26	11	23.9	8	2	Q9RQ57
27	11	23.9	8	2	Q9RQ49
28	11	23.9	8	4	Q9R7T2
29	11	23.9	8	4	Q9UHK1
30	11	23.9	8	4	Q9UDZ4
31	11	23.9	8	4	Q9BYI5
32	11	23.9	8	6	O02831
33	11	23.9	8	6	Q9BFC3
34	11	23.9	8	6	Q9BFC2
35	11	23.9	8	6	Q9BFC1
36	11	23.9	8	6	Q9BFC0
37	11	23.9	8	6	Q9BFB9
38	11	23.9	8	6	Q9BFB8
39	11	23.9	8	6	Q9BFB7
40	11	23.9	8	6	Q9BFB6
41	11	23.9	8	6	Q9BFB5
42	11	23.9	8	6	Q9BFB4
43	11	23.9	8	6	Q9BFB3
44	11	23.9	8	6	Q9BFB2
45	11	23.9	8	6	Q9BFB1

ALIGNMENTS

RESULT 1
P82445 PRELIMINARY; PRT; 7 AA.
ID P82445 PRELIMINARY; PRT; 7 AA.
AC P82445;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 10 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBITaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT 'Proteomic study of secondary cell wall proteins from transformed tobacco culture.';
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 7
SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;
Query Match 52.2%; Score 24; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 6.7e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 VRIGHLY 7
Db 1 VTGVHVF 7
RESULT 2
Q14277 PRELIMINARY; PRT; 9 AA.
ID Q14277 PRELIMINARY; PRT; 9 AA.

AC Q14277;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE RET protein short form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94071887; PubMed=7902707;
RA Ceccherini I., Bocciardi R., Luo Y., Pasini B., Hofstra R.,
RA Takahashi M., Romeo G.;
RT "Exon structure and flanking intronic sequences of the human RET
RT proto-oncogene.";
RL Biochem. Biophys. Res. Commun. 196:1288-1295(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94366753; PubMed=8084609;
RA Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
RA Bocciardi R., Nijveen H., Bolino A., Seri M., Ronchetto P., Pasini B.,
RA Bozzano M., Buys C., Romeo G.;
RT "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
RT the ret proto-oncogene.";
RL Oncogene 9:3025-3029(1994).
DR EMBL; U11532; AAC50102.1; -.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;

Query Match 41.3%; Score 19; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RIGHTLY 7
| | | | |
Db 1 RISHAF 6

RESULT 3
Q9YQ10 ID Q9YQ10 PRELIMINARY; PRT; 7 AA.
AC Q9YQ10;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical fusion protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99099045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes.";
RL J. Virol. 73:1535-1545(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95159435; PubMed=7856095;
RA Eleouet J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.;
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1
RT of transmissible gastroenteritis virus.";
RL Virology 206:817-822(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88078100; PubMed=2825819;
RA Rasschaert D., Gelfi J., Laude H.;
RT "Enteric coronavirus TGEV: partial sequence of the genomic RNA its
RT organization and expression.";
RL Biochimie 69:591-600(1987).

DR EMBL; AJ011482; CAA09625.1; -.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 37.0%; Score 17; DB 12; Length 7;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LYIL 9
| | | | |
Db 2 LYLL 5

RESULT 4
Q93SP2 ID Q93SP2 PRELIMINARY; PRT; 8 AA.
AC Q93SP2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Quaternary ammonium compound-resistance protein QacEdelta
DE (Fragment).
CN QACEDELTA1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YMC704; TRANSPOSON-CLASS I INTEGRON;
RA Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
RT "VIM-2 metallo-beta-lactamase gene-containing integron in a
RT Pseudomonas aeruginosa clinical isolate.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029772; AAK50441.1; -.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

Query Match 34.8%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GHLYL 9
| | | | |
Db 3 GVLFL 8

RESULT 5
Q9XNP8 ID Q9XNP8 PRELIMINARY; PRT; 8 AA.
AC Q9XNP8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ATP synthase 6 (Fragment).
GN ATP6.
OS Boophilus microplus (Cattle tick).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N;
RX MEDLINE=99297341; PubMed=10368952;
RA Campbell N.J.H., Barker S.C.;
RT "The novel mitochondrial gene arrangement of the cattle tick,
RT Boophilus microplus: fivefold tandem repetition of a coding region.";
RL Mol. Biol. Evol. 16:732-740(1999).
DR EMBL; AF110616; AAD28386.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 938 MW; 58BB14404B5735B0 CRC64;

4

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Query Match      32.6%; Score 15; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LYI 8
   |||
Db 3 LYI 5

RESULT 6
Q47410
ID Q47410 PRELIMINARY; PRT; 9 AA.
AC Q47410;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Pot. repAX peptide (Fragment).
OS Escherichia coli.
OG Plasmid NR1.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PLASMID NR1;
RX Womble D.D., Sampathkumar P., Easton A.M., Luckow V.A., Rownd R.H.;
RT "transcription of the replication control region of the IncFII R-
   plasmid NR1 in vitro and in vivo.";
RL J. Mol. Biol. 181:395-410(1985).
DR EMBL; X02302; CAA26166.1; -.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 9 AA; 1055 MW; DCF6A6412CDD1E87D CRC64;

Query Match      30.4%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GH 5
   ||
Db 3 GH 4

RESULT 7
Q9VW82
ID Q9VW82 PRELIMINARY; PRT; 9 AA.
AC Q9VW82;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE CG18219 protein (Fragment).
GN CG18219.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
   Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
   Abril J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
   Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
   Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,
   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
   RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003526; AAF49437.1; -.
DR FlyBase; FBgn0036647; CG18219.
FT NON_TER
SQ SEQUENCE 9 AA; 975 MW; F31AB4472045B9C1 CRC64;

Query Match      30.4%; Score 14; DB 5; Length 9;
Best Local Similarity 60.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 HLYIL 9
   | | |
Db 2 HFSIL 6

RESULT 8
O08979
ID O08979 PRELIMINARY; PRT; 9 AA.
AC O08979;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AML1 protein (Fragment).
GN AML1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=MURINE RETROVIRUS INDUCED TUMOR;
RX MEDLINE=9732339; PubMed=9188573;
RA Antoft H.W., Sorensen A.B., Barell C., Schmidt J., Luz A.,
   Pedersen F.S.;
RT "Stability of AML1 (core) site enhancer mutations in T-lymphomas
   induced by attenuated SL3-3 murine leukemia virus mutants.";
RL J. Virol. 71:5080-5087(1997).
DR EMBL; Y11802; CAA72496.1; -.
FT NON_TER
SQ SEQUENCE 9 AA; 981 MW; 293E01E865A776D8 CRC64;

Query Match      30.4%; Score 14; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GH 5

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Db          6 GH 7
||
RESULT 9
Q63480
ID Q63480 PRELIMINARY; PRT; 7 AA.
AC Q63480;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TR4-NS orphan receptor (Fragment).
GN TR4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96198747; PubMed=8612486;
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
RA Detera-Wadleigh S.D.;
RT "Splice variants of rat TR4 orphan receptor: differential expression
RT of novel sequences in the 5'-untranslated region and C-terminal
RT domain.";
RL Endocrinology 137:1562-1571(1996).
DR EMBL; U59125; AAB02827.1; -.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;

Query Match 28.3%; Score 13; DB 11; Length 7;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VRIGHL 6
|||
Db 2 IRGGDL 7

RESULT 10
Q9UMC7
ID Q9UMC7 PRELIMINARY; PRT; 8 AA.
AC Q9UMC7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE SHMT protein (Fragment).
GN SHMT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chave K.J., Snell K., Sanders P.G.;
RT "Isolation and characterisation of human genomic sequences encoding
RT cytosolic serine hydroxymethyltransferase.";
RL Biochem. Soc. Trans. 25:53-53(1997).
DR EMBL; Y14492; CAB54844.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 868 MW; 7C205721E44AB5B8 CRC64;

Query Match 28.3%; Score 13; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 HLXI 8
|||
Db 5 HLIL 8
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RESULT 11
Q34909
ID Q34909 PRELIMINARY; PRT; 8 AA.
AC Q34909;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome b (Fragment).
OS Locusta migratoria (Migratory locust).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridoidea; Acrididae; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88223478; PubMed=2836084;
RA McCracken A., Uhlenbusch I., Gellissen G.;
RT "Structure of the cloned Locusta migratoria mitochondrial genome:
RT restriction mapping and sequence of its ND-1 (URF-1) gene.";
RL Curr. Genet. 11:625-630(1987).
DR EMBL; X05286; CAA28905.1; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 28.3%; Score 13; DB 8; Length 8;
Best Local Similarity 20.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VRIGH 5
|||
Db 4 IKLKH 8

RESULT 12
Q8WGC7
ID Q8WGC7 PRELIMINARY; PRT; 8 AA.
AC Q8WGC7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE NADH dehydrogenase subunit 1 (Fragment).
OG Petrolisthes armatus (green porcelain crab).
OS Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
OC Galatheoidea; Porcellanidae; Petrolisthes.
OX NCBI_TaxID=84662;
RN [1]
RP SEQUENCE FROM N.A.
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondrial gene rearrangements support a hypothesis of parallel
RT evolution to the crab-like form.";
RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF436049; AAL31623.1; -.
KW Mitochondrion.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 1010 MW; FE20504B54472696 CRC64;

Query Match 28.3%; Score 13; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 YIL 9
|||
Db 5 YII 7

RESULT 13
Q83332
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ID Q83332 PRELIMINARY; PRT; 8 AA.
AC Q83332;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE Hemagglutinin-esterase (Fragment).
OS murine hepatitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11138;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JHM;
RX MEDLINE=95191005; PubMed=7884877;
RA Kim K.H., Makino S.;
RT "Two murine coronavirus genes suffice for viral RNA synthesis.";
RL J. Virol. 69:2313-2321(1995).
DR EMBL; U19933; AAA69002.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 907 MW; 92273B5B1735A2CD CRC64;

Query Match 28.3%; Score 13; DB 12; Length 8;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 YIL 9
Db 6 YLL 8

RESULT 14
P83222 PRELIMINARY; PRT; 9 AA.
AC P83222;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 34 kDa extracellular nuclease (EC 3.-.-.-) (Fragment).
OS Streptomyces antibioticus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1890;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, SUBCELLULAR LOCATION, AND
RP DEVELOPMENTAL STAGE.
RC STRAIN=ATCC 11891;
RX MEDLINE=99329048; PubMed=10400660;
RA Nicieza R.G., Huergo J., Connolly B.A., Sanchez J.;
RT "Purification, characterization, and role of nucleases and serine
RT proteases in Streptomyces differentiation. Analogies with the
RT biochemical processes described in late steps of eukaryotic
RT apoptosis.";
RL J. Biol. Chem. 274:20366-20375(1999).
CC -1- FUNCTION: INVOLVED IN DNA DEGRADATION IN THE SUBSTRATE MYCELIUM.
CC CUTS DNA NONSPECIFICALLY. POSSESSES ENDONUCLEOLYTIC ACTIVITY.
CC -1- ENZYME REGULATION: STIMULATED BY MAGNESIUM AND MANGANESE.
CC INHIBITED BY ZINC AND AURIN TRICARBOXYLIC ACID.
CC -1- SUBUNIT: MONOMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- DEVELOPMENTAL STAGE: HIGHEST EXPRESSION FOUND DURING AERIAL
CC MYCELIUM FORMATION AND SPORULATION.
CC -1- MISCELLANEOUS: OPTIMUM PH IS 8-8.5.
KW Hydrolase; Nuclease; Magnesium.
FT UNSURE 1 1 OR E.
FT UNSURE 5 5 OR A.
FT NON_TER 9
SQ SEQUENCE 9 AA; 994 MW; 80B05AB6D8705731 CRC64;

Query Match 28.3%; Score 13; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
Oy 3 IGHLY 7
Db 4 IGQDY 8

RESULT 15
Q9UQA3 PRELIMINARY; PRT; 9 AA.
AC Q9UQA3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE p27kip1 protein (Fragment).
GN p27Kip1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99173873; PubMed=10072762;
RA Ito E., Iwahashi Y., Yanagisawa Y., Suzuki Y., Sugano S., Yuasa Y.,
RA Maruyama K.;
RT "Two short sequences have positive effects on the human p27(Kip1) gene
RT transcription.";
RL Gene 228:93-100(1999).
DR EMBL; AB005590; BAA76715.1; -.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 963 MW; 984D5A2D412C455 CRC64;

Query Match 28.3%; Score 13; DB 4; Length 9;
Best Local Similarity 40.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VRIGH 5
Db 4 VRVSN 8

Search completed: December 19, 2002, 16:44:41
Job time : 60 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:38:38 ; Search time 56 Seconds
(without alignments)
21.415 Million cell updates/sec

Title: US-09-692-401-4
Perfect score: 46
Sequence: 1 VRIGHLYIL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 130868

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002.*
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	9	AAE12995	Human MAGE-12 T-ce
2	46	100.0	9	AAE02082	MAGE-A12 human leu
3	42	91.3	8	AAE02084	MAGE-A12 human leu
4	38	82.6	9	AAE02083	MAGE-21 nonapeptid
5	38	82.6	9	AAE02084	MAGE-21 nonapeptid
6	38	82.6	9	AAE02084	MAGE-21 nonapeptid
7	38	82.6	9	AAE02084	MAGE-21 nonapeptid
8	35	76.1	9	AAE02081	MAGE-A12 human leu
9	35	76.1	9	AAE02081	MAGE-A12 human leu
10	33	71.7	9	AAE02081	MAGE-A12 human leu

11	33	71.7	9	20	AAE02082	Immunogenic peptid
12	33	71.7	9	20	AAE02083	Immunogenic peptid
13	33	71.7	9	20	AAE02083	Immunogenic peptid
14	33	71.7	9	20	AAE02083	Immunogenic peptid
15	33	71.7	9	20	AAE02083	Immunogenic peptid
16	33	71.7	9	20	AAE02083	Immunogenic peptid
17	33	71.7	9	20	AAE02083	Immunogenic peptid
18	33	71.7	9	20	AAE02083	Immunogenic peptid
19	33	71.7	9	20	AAE02083	Immunogenic peptid
20	33	71.7	9	20	AAE02083	Immunogenic peptid
21	33	71.7	9	20	AAE02083	Immunogenic peptid
22	33	71.7	9	20	AAE02083	Immunogenic peptid
23	33	71.7	9	20	AAE02083	Immunogenic peptid
24	33	71.7	9	20	AAE02083	Immunogenic peptid
25	33	71.7	9	20	AAE02083	Immunogenic peptid
26	33	71.7	9	20	AAE02083	Immunogenic peptid
27	33	71.7	9	20	AAE02083	Immunogenic peptid
28	33	71.7	9	20	AAE02083	Immunogenic peptid
29	33	71.7	9	20	AAE02083	Immunogenic peptid
30	33	71.7	9	20	AAE02083	Immunogenic peptid
31	33	71.7	9	20	AAE02083	Immunogenic peptid
32	33	71.7	9	20	AAE02083	Immunogenic peptid
33	33	71.7	9	20	AAE02083	Immunogenic peptid
34	33	71.7	9	20	AAE02083	Immunogenic peptid
35	33	71.7	9	20	AAE02083	Immunogenic peptid
36	33	71.7	9	20	AAE02083	Immunogenic peptid
37	33	71.7	9	20	AAE02083	Immunogenic peptid
38	33	71.7	9	20	AAE02083	Immunogenic peptid
39	33	71.7	9	20	AAE02083	Immunogenic peptid
40	33	71.7	9	20	AAE02083	Immunogenic peptid
41	33	71.7	9	20	AAE02083	Immunogenic peptid
42	33	71.7	9	20	AAE02083	Immunogenic peptid
43	33	71.7	9	20	AAE02083	Immunogenic peptid
44	33	71.7	9	20	AAE02083	Immunogenic peptid
45	33	71.7	9	20	AAE02083	Immunogenic peptid

ALIGNMENTS

RESULT 1	AAE12995	AAE12995 standard; peptide; 9 AA.
ID	AAE12995	AAE12995 standard; peptide; 9 AA.
XX	AAE12995	
AC	AAE12995	
XX	AAE12995	
DT	28-JAN-2002	(first entry)
XX	Human MAGE-12	T-cell epitope.
DE	Human MAGE-12	T-cell epitope.
XX	Human MAGE-12	T-cell epitope.
KW	Human MAGE-12	T-cell epitope.
KW	Human MAGE-12	T-cell epitope.
OS	Human MAGE-12	T-cell epitope.
PN	Human MAGE-12	T-cell epitope.
XX	Human MAGE-12	T-cell epitope.
PD	Human MAGE-12	T-cell epitope.
XX	Human MAGE-12	T-cell epitope.
PF	Human MAGE-12	T-cell epitope.
XX	Human MAGE-12	T-cell epitope.
PR	Human MAGE-12	T-cell epitope.
XX	Human MAGE-12	T-cell epitope.
PA	Human MAGE-12	T-cell epitope.
XX	Human MAGE-12	T-cell epitope.
XX	Human MAGE-12	T-cell epitope.
DR	Human MAGE-12	T-cell epitope.
XX	Human MAGE-12	T-cell epitope.
PT	Human MAGE-12	T-cell epitope.
PT	Human MAGE-12	T-cell epitope.

Novel T cell epitope of MAGE-12 is a tumor rejection antigen for a melanoma expressing HLA-Cw0702 recognized by tumor-infiltrating lymphocytes and useful to treat cancer particularly melanoma

XX Claim 1; Page 14; 17pp; English.

XX The invention relates to an isolated and purified T cell epitope of

CC MAGE-12. MAGE-12 is a tumour rejection antigen for melanoma which

CC expresses MHC-class I molecule HLA-Cw0702 recognised by tumour-

CC infiltrating lymphocytes. The epitope or a vector encoding the epitope

CC is used to treat cancer, particularly melanoma expressing HLA-Cw

CC asterisk 0702. The epitope has widespread utility in cancer immunotherapy

CC since MAGE-12 is mostly found in tumours. The present sequence is

CC human MAGE-12 T-cell epitope.

XX Sequence 9 AA;

SQ Query Match 100.0%; Score 46; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLYIL 9

Db 1 VRIGHLYIL 9

RESULT 2

AAE02082

ID AAE02082 standard; peptide; 9 AA.

XX AC AAE02082;

XX 31-JUL-2001 (first entry)

XX MAGE-A12 human leukocyte antigen-binding peptide #2.

XX Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;

KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;

KW brain tumour; sarcoma; vaccine; gene therapy.

XX Homo sapiens.

OS WO200129220-A2.

XX 26-APR-2001.

XX 19-OCT-2000; 2000WO-US28852.

PF 19-OCT-1999; 99US-0160374.

PR 01-FEB-2000; 2000US-0179570.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;

PI WPI; 2001-328498/34.

XX New antigenic peptides derived from MAGE-A12 polypeptides, useful for

PT diagnosis and treatment of cancer, such as bladder, lung, breast,

PT brain, prostate and renal carcinomas -

XX Claim 2; Page 42; 69pp; English.

XX The patent discloses antigenic peptides derived from MAGE-A12

CC protein and presented by human leukocyte antigens (HLAs). These

CC antigenic peptides when presented by an antigen presenting cell

CC having a HLA class I molecule, effectively induce the activation

CC and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is

CC useful for treating a subject having a disorder characterised by

CC expression of MAGE-A12. The protein microarray comprising MAGE-A12

CC is useful for diagnosing a disorder, especially cancer, by determining

CC the binding of an antibody, T lymphocytes or a HLA molecule isolated

CC from the subject suspected of having the disorder characterised by the

CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,

CC including bladder carcinomas, melanomas, oesophageal, lung, head and

CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,

CC antibodies are useful for diagnosing disorders characterised by

CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-12 peptides

CC are used as vaccines. They are also used in gene therapy.

CC prostate and renal carcinomas and to produce antibodies. MAGE-A12

CC antibodies are useful for diagnosing disorders characterised by

CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-12 peptides

CC are used as vaccines. They are also used in gene therapy.

CC The present sequence is MAGE-A12 HLA class-I-binding peptide. This

CC antigenic peptide is presented by major histocompatibility complex

CC (MHC) and is recognised by CTLs.

XX Sequence 9 AA;

SQ Query Match 100.0%; Score 46; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLYIL 9

Db 1 VRIGHLYIL 9

RESULT 3

AAE02084

ID AAE02084 standard; peptide; 8 AA.

XX AC AAE02084;

XX 31-JUL-2001 (first entry)

XX MAGE-A12 human leukocyte antigen-binding peptide #4.

XX Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;

KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;

KW brain tumour; sarcoma; vaccine; gene therapy.

XX Homo sapiens.

OS WO200129220-A2.

XX 26-APR-2001.

XX 19-OCT-2000; 2000WO-US28852.

PF 19-OCT-1999; 99US-0160374.

PR 01-FEB-2000; 2000US-0179570.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;

PI WPI; 2001-328498/34.

XX New antigenic peptides derived from MAGE-A12 polypeptides, useful for

PT diagnosis and treatment of cancer, such as bladder, lung, breast,

PT brain, prostate and renal carcinomas -

XX Claim 1; Page 43; 69pp; English.

XX The patent discloses antigenic peptides derived from MAGE-A12

CC protein and presented by human leukocyte antigens (HLAs). These

CC antigenic peptides when presented by an antigen presenting cell

CC having a HLA class I molecule, effectively induce the activation

CC and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is

CC useful for treating a subject having a disorder characterised by

CC expression of MAGE-A12. The protein microarray comprising MAGE-A12

CC is useful for diagnosing a disorder, especially cancer, by determining

CC the binding of an antibody, T lymphocytes or a HLA molecule isolated

CC from the subject suspected of having the disorder characterised by the

CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,

CC including bladder carcinomas, melanomas, oesophageal, lung, head and

CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,

CC prostate and renal carcinomas and to produce antibodies. MAGE-A12

CC antibodies are useful for diagnosing disorders characterised by

CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-12 peptides

CC are used as vaccines. They are also used in gene therapy.

CC The present sequence is MAGE-A12 HLA Class-I-binding peptide. This
 CC antigenic peptide is presented by major histocompatibility complex
 CC (MHC) and is recognised by CTLs.

XX SQ Sequence 8 AA;

Query Match 91.3%; Score 42; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RIGHLYIL 9
 |
 Db 1 RIGHLYIL 8
 |

RESULT 4

AAR50283
 ID AAR50283 standard; Protein; 9 AA.

XX AC AAR50283;

XX DT 26-SEP-1994 (first entry)

XX DE MAGE-21 nonapeptide.

XX KW MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;
 KW histocompatibility; human leucocyte antigen; probe; treatment;
 KW therapy; vaccine.

XX OS Synthetic.

XX PN WO9405304-A.

XX PD 17-MAR-1994.

XX PF 30-AUG-1993; 93WO-US08157.

XX PR 31-AUG-1992; 92US-0938334.

XX PR 26-MAR-1993; 93US-0037230.

XX PR 07-JUN-1993; 93US-0073103.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Boon-falleur T, De Plaen E, Lurquin C, Traversari C;

XX PI Van Derbruggen P;

XX DR WPI; 1994-100844/12.

XX DR N-PSDB; AAQ44753.

XX PS New nona:peptide derived from tumour rejection antigen precursor

PT - presented by HLA-A1 cancer cells, for use in diagnosis or
 PT therapy of esp. melanoma and breast cancer.

XX PS Disclosure; Page 20; 33pp; English.

XX CC An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-
 CC Pro-Tle-Gly-His-Leu-Tyr is derived from the tumour rejection antigen
 CC precursor encoded by the MAGE-3 gene and presented by HLA-A1. The
 CC nonapeptide can be used in a vaccine to treat a cancerous condition
 CC involving HLA-A1 subtype cancerous cells. The nucleic acid encoding
 CC the nonapeptide can be used as a probe to identify tumour cells.

XX CC This sequence is homologous to the peptide described and is encoded
 CC by the MAGE-21 gene.

XX SQ Sequence 9 AA;

Query Match 82.6%; Score 38; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
 |
 Db 3 VRIGHLY 9
 |

RESULT 5

AAR99345
 ID AAR99345 standard; Protein; 9 AA.

XX AC AAR99345;

XX DT 22-APR-1997 (first entry)

XX DE MAGE-21 nonapeptide.

XX KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
 KW tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
 KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
 KW therapy.

XX OS Homo sapiens.

XX PN WO9626214-A1.

XX PD 29-AUG-1996.

XX PF 01-FEB-1996; 96WO-US01489.

XX PR 23-FEB-1995; 95US-0393273.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;

XX PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;

XX DR WPI; 1996-402317/40.

XX DR N-PSDB; AAT35410.

XX PT New nona:peptide(s) that bind to HLA molecule(s) and induce lysis
 PT by specific cytolytic T cells, for diagnosis and treatment of
 PT tumours and to expand T cells in vitro.

XX PS Example 4; Fig 4; 41pp; English.

XX CC AAR99343-R99350 represent MAGE nonapeptides, based on the tumour
 CC rejection antigen region of the full length MAGE sequences. These
 CC peptides were used to design the nonapeptides of the invention (see
 CC AAR99337-R99342), which bind to a HLA molecule on a cell, and provoke
 CC lysis by cytolytic T cells (CTLs) specific for a complex of the HLA
 CC molecule and nonapeptide. The nonapeptides can be used diagnostically to
 CC identify tumours expressing a particular HLA molecule, or to identify
 CC cancer cells. The peptides can also be used therapeutically, to induce a
 CC CTL response to tumours (where the peptides are optionally coupled to
 CC tumour-specific antibodies), or to induce a response by CTLs that are
 CC otherwise inactive. The peptide sequences may also be used to expand
 CC specific CTLs in vitro for later return to the patient, such as for
 CC treating melanoma. Tumour cells can be identified by using DNA encoding
 CC the nonapeptides as probes. Non-human cells transformed with the HLA-A1
 CC gene and a DNA sequence encoding one of the peptides, can be used to
 CC generate CTLs, or to detect the presence of CTLs in human samples. The
 CC non-human transformed cells, when polytransformed, are universal effector
 CC cells, and can be used in vaccines, or for treating melanoma or breast
 CC cancer.

XX SQ Sequence 9 AA;

Query Match 82.6%; Score 38; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
 |
 Db 3 VRIGHLY 9
 |

RESULT 6

AAAY46062
ID AAY46062 standard; Peptide; 9 AA.

XX AC
XX DT
XX DT

DT 01-DEC-1999 (first entry)

XX Immunogenic peptide having a human leukocyte antigen binding motif #673.
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.

XX Synthetic.
XX Homo sapiens.
XX WO945954-A1.

XX 16-SEP-1999.

XX PF 13-MAR-1998; 98WO-US05039.

XX PR 13-MAR-1998; 98WO-US05039.

XX PA (EPIM-) EPIMMUNE INC.

XX PI Sette A, Kubo RT, Sidney J, Cellis E, Grey HM, Southwood S;

XX WPI; 1999-551214/46.

XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -

PS Claim 1; Page 54; 150pp; English.

XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.

XX Sequence 9 AA;

Query Match 82.6%; Score 38; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
| | | | |
Db 3 VRIGHLY 9

RESULT 7

AAE02081
ID AAE02081 standard; peptide; 9 AA.

XX AAE02081;

XX 31-JUL-2001 (first entry)

DE MAGE-A12 human leukocyte antigen-binding peptide #1.

XX Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
KW brain tumour; sarcoma; vaccine; gene therapy.

XX Homo sapiens.

XX WO200129220-A2.

XX 26-APR-2001.

XX PF 19-OCT-2000; 2000WO-US28852.

XX PR 19-OCT-1999; 99US-0160374.

XX PR 01-FEB-2000; 2000US-0179570.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;

XX WPI; 2001-328498/34.

XX New antigenic peptides derived from MAGE-A12 polypeptides, useful for
XX diagnosis and treatment of cancer, such as bladder, lung, breast,
XX brain, prostate and renal carcinomas -

XX Example 1; Page 42; 69pp; English.

XX The patent discloses antigenic peptides derived from MAGE-A12
CC protein and presented by human leukocyte antigens (HLAs). These
CC antigenic peptides when presented by an antigen presenting cell
CC having a HLA class I molecule, effectively induce the activation
CC and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is
CC useful for treating a subject having a disorder characterised by
CC expression of MAGE-A12. The protein microarray comprising MAGE-A12
CC is useful for diagnosing a disorder, especially cancer, by determining
CC the binding of an antibody, T lymphocytes or a HLA molecule isolated
CC from the subject suspected of having the disorder characterised by the
CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,
CC including bladder carcinomas, melanomas, oesophageal, lung, head and
CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
CC prostate and renal carcinomas and to produce antibodies. MAGE-A12
CC antibodies are useful for diagnosing disorders characterised by
CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-A12 peptides
CC are used as vaccines. They are also used in gene therapy.
CC The present sequence is MAGE-A12 HLA class-I-binding peptide. This
CC antigenic peptide is presented by major histocompatibility complex
CC (MHC) and is recognised by CTLs.

XX Sequence 9 AA;

Query Match 82.6%; Score 38; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
| | | | |
Db 3 VRIGHLY 9

RESULT 8

AAG84743
ID AAG84743 standard; Peptide; 9 AA.

XX AAG84743;

XX 10-SEP-2001 (first entry)

XX DE MAGE3 HLA-B7 supermotif-bearing peptide #9.
 DE XE Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte;
 KW CTL; MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine;
 KW cancer; cytostatic; immunostimulant.
 XX OS Homo sapiens.
 OS Synthetic.
 XX WO200142267-A1.
 PN 14-JUN-2001.
 XX 11-DEC-2000; 2000WO-US33545.
 PF 10-DEC-1999; 99US-0458298.
 PR (EPIM-) EPIMMUNE INC.
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 XX WPI; 2001-375002/39.
 DR An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
 PT the treatment and prevention of cancer -
 XX Claim 1; Page 156; 17lpp; English.
 XX The present invention describes MAGE2/3 epitopes (I). Also described
 CC are: (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo
 CC and binds to a complex of (I); (2) a peptide (II) comprising (I) and a
 CC second epitope and has less than 50 contiguous amino acids; (3) a vaccine
 CC composition comprising (II), a unit dose of a peptide with at least 50
 CC contiguous amino acids with 100% identity to the native peptide sequence
 CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
 CC encoding (I); and (5) an isolated nucleic acid encoding (II). (I) has
 CC cytostatic activity, and can be used in vaccines and as an
 CC immunostimulant. A vaccine of (3) is useful for the treatment and
 CC prevention of cancer. (I) is useful for monitoring or evaluating an
 CC immune response by incubating a T-lymphocyte sample from a patient with
 CC (I) that binds to an human leukocyte antigen (HLA) allele present in the
 CC patient and detecting the presence of the T-lymphocyte that binds to the
 CC peptide. The vaccine allows the opportunity to combine epitopes derived
 CC from multiple tumour-associated molecules reducing the likelihood of
 CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAB99725
 CC represent amino acid sequences used in the exemplification of the
 CC present invention.
 XX SQ Sequence 9 AA;
 Query Match 76.1%; Score 35; DB 22; Length 9;
 Best Local Similarity 85.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 IGHLYIL 9
 Db 3 IGHLYII 9
 RESULT 9
 AAB76152
 ID AAB76152 standard; Peptide; 9 AA.
 XX AAB76152;
 AC AAB76152;
 XX 10-APR-2001 (first entry)
 DT Tumour associated antigen MAGE3 immunogenic peptide.
 XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic.

KW HLA binding peptide; immune response; glycoprotein; cytostatic;
 KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
 KW human immunodeficiency virus; protozoacide; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
 KW condyloma acuminatum.
 XX Homo sapiens.
 OS WO200100225-A1.
 PN 04-JAN-2001.
 XX 28-JUN-2000; 2000WO-US17842.
 PF 29-JUN-1999; 99US-0141422.
 PR (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S;
 PI WPI; 2001-112389/12.
 XX Composition comprising human leukocyte antigen binding peptide which
 PT comprises isolated, prepared epitope useful for treating viral
 PT infections such as acquired immunodeficiency syndrome, and cancer -
 XX Claim 1; Page 48; 58pp; English.
 XX The present invention describes a composition (I) which comprises at
 CC least one human leukocyte antigen (HLA) binding peptide comprising an
 CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
 CC sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic,
 CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
 CC immunodeficiency virus) and protozoacide activities, which can be used
 CC in vaccine production and is an inducer of cytotoxic T-cell response.
 CC (I) is useful for inducing a cytotoxic T cell response against a
 CC preselected antigen in a patient expressing a specific major
 CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic
 CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
 CC treat and/or prevent viral infection and cancer such as prostate cancer,
 CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
 CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
 CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
 CC acuminatum.
 XX SQ Sequence 9 AA;
 Query Match 76.1%; Score 35; DB 22; Length 9;
 Best Local Similarity 85.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 IGHLYIL 9
 Db 3 IGHLYII 9
 RESULT 10
 AAW45704
 ID AAW45704 standard; peptide; 9 AA.
 XX AAW45704;
 AC AAW45704;
 XX 09-JUN-1998 (first entry)
 DT MAGE-2 170 peptide with binding affinity for HLA-B7-like molecules.
 XX HLA molecule; cytotoxic T cell; immunogenic peptide; binding affinity;
 KW HLA-B7 supermotif; tumour; infection; parasite; CTL; antigen; melanoma;
 KW MAGE-2.
 XX Synthetic.

OS Homo sapiens.
 XX WO9733602-A1.
 PN
 XX 18-SEP-1997.
 PD
 XX 10-MAR-1997; 97WO-US03778.
 PF
 XX 11-MAR-1996; 96US-0013113.
 PR
 XX (CYTE-) CYTEL CORP.
 PA
 PI Chestnut RW, Sette A, Sidney J;
 XX WPI; 1997-470637/43.
 DR
 XX Inducing cytotoxic T cell response against specific antigen - using
 PT immunogenic peptide with binding affinity for HLA-A3-like molecules,
 PT to treat or prevent tumours and infections by virus, parasites etc
 XX
 PS Example 2; Page 51; 79pp; English.
 XX
 CC This sequence represents an immunogenic peptide with binding affinity
 CC for HLA-B7-like molecules. A cytotoxic T cell (CTL) response against a
 CC particular antigen (Ag) is induced in a patient by contacting a CTL with
 CC an immunogenic peptide of 9-15 amino acids which binds to at least two
 CC HLA-A3-like molecules with dissociation constant less than 500 nM and
 CC induces a cytotoxic T cell response. The immunogenic peptide has a
 CC sequence of 9 amino acids, comprising a binding motif, with from the
 CC N-to C-termini: primary anchor sites (PAR) at positions 2 (selected from
 CC Ala, Leu, Ile, Val, Met, Ser or Thr) and 9 (Arg or Lys) and at least one
 CC secondary anchor sites (SAR), i.e. Tyr, Phe or Trp at positions 3, 6 or
 CC 7, and/or Pro at position 8. The immunogenic peptides are used in peptide
 CC based vaccines and therapeutic compositions, for treating viral,
 CC parasitic or fungal diseases or cancer, e.g. prostatic cancer, hepatitis
 CC B or C, renal or cervical carcinoma, lymphoma, cytomegalovirus infection
 CC or condyloma acuminatum. They can also be used to elicit a CTL response
 CC in vitro for subsequent return of the cells to the patient, e.g. where
 CC the patient does not respond to peptide vaccines or other therapies.
 CC Selection of specific residues for PAR and SAR results in higher binding
 CC affinity and thus increased immunogenicity.
 XX
 SQ Sequence 9 AA;
 Query Match 71.7%; Score 33; DB 18; Length 9;
 Best Local Similarity 77.8%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VRIGHLYIL 9
 | | | | |
 DB 1 VPISHLYIL 9
 RESULT 11
 AAY46232
 ID AAY46232 standard; Peptide; 9 AA.
 XX
 AC AAY46232;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #843.
 XX
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 PD 16-SEP-1999.

XX
 PD 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98WO-US05039.
 XX
 PR 13-MAR-1998; 98WO-US05039.
 XX
 PA (EPTM-) EPTM INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX WPI; 1999-551214/46.
 DR
 XX New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 XX
 PS Claim 1; Page 62; 150pp; English.
 XX
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The peptides are
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 9 AA;
 Query Match 71.7%; Score 33; DB 20; Length 9;
 Best Local Similarity 77.8%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VRIGHLYIL 9
 | | | | |
 DB 1 VPISHLYIL 9
 RESULT 12
 AAY46263
 ID AAY46263 standard; Peptide; 9 AA.
 XX
 AC AAY46263;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #874.
 XX
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 PD 16-SEP-1999.

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XX PF 13-MAR-1998; 98WO-US05039.
XX XX
XX PR 13-MAR-1998; 98WO-US05039.
XX XX
XX PA (EPIM-) EPIMMUNE INC.
XX XX
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX XX
XX DR WPI; 1999-551214/46.
XX XX
XX PT New immunogenic peptides with HLA binding motif, useful in treatment
XX PT and diagnosis of cancers and viral diseases
XX PS Claim 1; Page 64; 150pp; English.
XX XX
XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also
XX CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX CC response against the antigen from which the peptide is derived.
XX CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX CC normally induced by an antigen in the form of a peptide fragment bound
XX CC to a HLA molecule, rather than the intact foreign antigen itself, and
XX CC are particularly important in tumour rejection and in fighting viral
XX CC infections. The peptides are therefore useful therapeutically to treat
XX CC or prevent viral infections and cancers in mammals (especially humans)
XX CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX CC They can be administered as vaccines to elicit an immune response in
XX CC individuals susceptible or otherwise at risk of viral infection or
XX CC cancer, or used to treat chronic or acute conditions. They are also
XX CC useful diagnostically, and can be used to induce a cytotoxic T cell
XX CC response, by contacting a cytotoxic T cell with the peptide e.g. to
XX CC produce CTLs ex vivo for infusion back into a patient. The
XX CC polynucleotides encoding the immunogenic peptides are also useful
XX CC therapeutically and for immunisation as above.
XX SQ Sequence 9 AA;

Query Match 71.7%; Score 33; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGHLYI 8
Db 3 IGHLYI 8

RESULT 13
AAY47329
ID AAY47329 standard; Peptide; 9 AA.
XX AC
XX AC AAY47329;
XX DT
XX DT 01-DEC-1999 (first entry)
XX DE
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1940.
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX KW immune response; T cell activation; major histocompatibility complex;
XX KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX KW vaccine; immunisation.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9945954-A1.
XX PN
XX PD 16-SEP-1999.
XX PD
XX PF 13-MAR-1998; 98WO-US05039.
XX PF
XX PR 13-MAR-1998; 98WO-US05039.
XX PR

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XX PR 13-MAR-1998; 98WO-US05039.
XX XX
XX XX (EPIM-) EPIMMUNE INC.
XX XX
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX XX
XX XX WPI; 1999-551214/46.
XX XX
XX PT New immunogenic peptides with HLA binding motif, useful in treatment
XX PT and diagnosis of cancers and viral diseases
XX PS Claim 1; Page 103; 150pp; English.
XX XX
XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also
XX CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX CC response against the antigen from which the peptide is derived.
XX CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX CC normally induced by an antigen in the form of a peptide fragment bound
XX CC to a HLA molecule, rather than the intact foreign antigen itself, and
XX CC are particularly important in tumour rejection and in fighting viral
XX CC infections. The peptides are therefore useful therapeutically to treat
XX CC or prevent viral infections and cancers in mammals (especially humans)
XX CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX CC They can be administered as vaccines to elicit an immune response in
XX CC individuals susceptible or otherwise at risk of viral infection or
XX CC cancer, or used to treat chronic or acute conditions. They are also
XX CC useful diagnostically, and can be used to induce a cytotoxic T cell
XX CC response, by contacting a cytotoxic T cell with the peptide e.g. to
XX CC produce CTLs ex vivo for infusion back into a patient. The
XX CC polynucleotides encoding the immunogenic peptides are also useful
XX CC therapeutically and for immunisation as above.
XX SQ Sequence 9 AA;

Query Match 71.7%; Score 33; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGHLYI 8
Db 2 IGHLYI 7

RESULT 14
AAY47944
ID AAY47944 standard; Peptide; 9 AA.
XX AC
XX AC AAY47944;
XX DT
XX DT 01-DEC-1999 (first entry)
XX DE
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2555.
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX KW immune response; T cell activation; major histocompatibility complex;
XX KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX KW vaccine; immunisation.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9945954-A1.
XX PN
XX PD 16-SEP-1999.
XX PD
XX PF 13-MAR-1998; 98WO-US05039.
XX PF
XX PR 13-MAR-1998; 98WO-US05039.
XX PR

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XX PA (EPIM-) EPIMMUNE INC.
XX PI
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX DR WPI; 1999-551214/46.
XX DR
XX PT New immunogenic peptides with HLA binding motif, useful in treatment
XX PT and diagnosis of cancers and viral diseases -
XX PS Claim 1; Page 128; 150pp; English.
XX PS
XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also
XX CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX CC response against the antigen from which the peptide is derived.
XX CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX CC normally induced by an antigen in the form of a peptide fragment bound
XX CC to a HLA molecule, rather than the intact foreign antigen itself, and
XX CC are particularly important in tumour rejection and in fighting viral
XX CC infections. The peptides are therefore useful therapeutically to treat
XX CC or prevent viral infections and cancers in mammals (especially humans)
XX CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX CC They can be administered as vaccines to elicit an immune response in
XX CC individuals susceptible or otherwise at risk of viral infection or
XX CC cancer, or used to treat chronic or acute conditions. They are also
XX CC useful diagnostically, and can be used to induce a cytotoxic T cell
XX CC response, by contacting a cytotoxic T cell with the peptide e.g. to
XX CC produce CTLs ex vivo for infusion back into a patient. The
XX CC polynucleotides encoding the immunogenic peptides are also useful
XX CC therapeutically and for immunisation as above.
XX SQ Sequence 9 AA;

Query Match 71.7%; Score 33; DB 20; Length 9;
Best Local Similarity 77.8%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VRIGHLYIL 9
Db 1 VPISHLYIL 9

RESULT 15
AAY47950
ID AAY47950 standard; Peptide; 9 AA.
XX AC AAY47950;
XX DT
XX DT 01-DEC-1999 (first entry)
XX DE
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2561.
XX KW Human leukocyte antigen; binding; Immunogenic; glycoprotein; MHC; HLA;
XX KW immune response; T cell activation; major histocompatibility complex;
XX KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX KW vaccine; immunisation.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN W05945954-A1.
XX PD 16-SEP-1999.
XX PF 13-MAR-1998; 98WO-US05039.
XX PR 13-MAR-1998; 98WO-US05039.
XX PA (EPIM-) EPIMMUNE INC.

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XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX DR WPI; 1999-551214/46.
XX DR
XX PT New immunogenic peptides with HLA binding motif, useful in treatment
XX PT and diagnosis of cancers and viral diseases -
XX PS Claim 1; Page 129; 150pp; English.
XX PS
XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also
XX CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX CC response against the antigen from which the peptide is derived.
XX CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX CC normally induced by an antigen in the form of a peptide fragment bound
XX CC to a HLA molecule, rather than the intact foreign antigen itself, and
XX CC are particularly important in tumour rejection and in fighting viral
XX CC infections. The peptides are therefore useful therapeutically to treat
XX CC or prevent viral infections and cancers in mammals (especially humans)
XX CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX CC They can be administered as vaccines to elicit an immune response in
XX CC individuals susceptible or otherwise at risk of viral infection or
XX CC cancer, or used to treat chronic or acute conditions. They are also
XX CC useful diagnostically, and can be used to induce a cytotoxic T cell
XX CC response, by contacting a cytotoxic T cell with the peptide e.g. to
XX CC produce CTLs ex vivo for infusion back into a patient. The
XX CC polynucleotides encoding the immunogenic peptides are also useful
XX CC therapeutically and for immunisation as above.
XX SQ Sequence 9 AA;

Query Match 71.7%; Score 33; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGHLYI 8
Db 3 IGHLYI 8

Search completed: December 19, 2002, 16:43:33
Job time : 64 secs

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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:45:03 ; Search time 11 Seconds
(without alignments)
13.716 Million cell updates/sec

Title: US-09-692-401-4
Perfect score: 46
Sequence: 1 VRIGHLYIL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues
Total number of hits satisfying chosen parameters: 17934

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	71.7	9	9	US-09-766-889A-58
2	33	71.7	9	9	US-09-017-743C-30
3	33	71.7	9	9	US-09-017-743C-67
4	31	67.4	9	9	US-09-017-743C-31
5	29	63.0	8	9	US-09-017-743C-100
6	29	63.0	9	9	US-09-766-889A-18
7	29	63.0	9	9	US-09-766-889A-56
8	29	63.0	9	9	US-09-909-460-51
9	29	63.0	9	10	US-09-812-528-3
10	29	63.0	9	10	US-09-847-185-23
11	29	63.0	9	10	US-09-923-831-6
12	28	60.9	9	9	US-09-017-743C-32
13	26	56.5	9	9	US-09-766-889A-7
14	26	56.5	9	12	US-10-026-001-3
15	24	52.2	9	10	US-09-894-018-319
16	23	50.0	9	9	US-09-826-290-24
17	23	50.0	9	9	US-09-826-290-95
18	23	50.0	9	9	US-09-017-743C-38
19	23	50.0	9	10	US-09-791-378-538

20	22	47.8	7	10	US-09-765-086-79	Sequence 79, Appl
21	21	45.7	7	10	US-09-730-801-1	Sequence 1, Appli
22	21	45.7	8	9	US-09-766-347-1	Sequence 1, Appli
23	21	45.7	8	10	US-09-756-875-16	Sequence 16, Appl
24	21	45.7	8	10	US-09-756-875-17	Sequence 17, Appl
25	21	45.7	9	10	US-09-756-983-6	Sequence 6, Appli
26	21	45.7	9	10	US-09-756-983-13	Sequence 13, Appl
27	20	43.5	9	10	US-09-729-835-123	Sequence 123, App
28	19	41.3	6	9	US-09-813-718-42	Sequence 42, Appl
29	19	41.3	7	8	US-08-812-393A-51	Sequence 51, Appl
30	19	41.3	7	9	US-10-080-100-86	Sequence 86, Appl
31	19	41.3	7	10	US-09-824-286-14	Sequence 14, Appl
32	19	41.3	7	10	US-09-731-242A-24	Sequence 24, Appl
33	19	41.3	7	10	US-09-901-187B-10	Sequence 10, Appl
34	19	41.3	8	9	US-09-766-889A-10	Sequence 10, Appl
35	19	41.3	8	10	US-09-071-838-45	Sequence 45, Appl
36	19	41.3	9	1	US-08-821-739A-34	Sequence 34, Appl
37	19	41.3	9	8	US-08-424-550B-266	Sequence 266, App
38	19	41.3	9	9	US-09-766-889A-8	Sequence 8, Appli
39	19	41.3	9	9	US-09-766-889A-16	Sequence 16, Appl
40	19	41.3	9	9	US-09-909-460-49	Sequence 49, Appl
41	19	41.3	9	9	US-09-909-460-91	Sequence 91, Appl
42	19	41.3	9	9	US-09-909-460-93	Sequence 93, Appl
43	19	41.3	9	10	US-09-812-528-1	Sequence 1, Appli
44	19	41.3	9	10	US-09-847-185-21	Sequence 21, Appl
45	19	41.3	9	10	US-09-839-497A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-766-889A-58
; Sequence 58, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-58

Query Match 71.7%; Score 33; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3	IGHLYI 8
Db	3	IGHLYI 8

RESULT 2

US-09-017-743C-30
; Sequence 30, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro

; Sidney, John
; Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-017-743C-30

Query Match 71.7%; Score 33; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 8.9e+04;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VRIGHLYIL 9
| | | | |
Db 1 VPISHLYIL 9

RESULT 3
US-09-017-743C-67
; Sequence 67, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; Sidney, John
; Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-017-743C-67

Query Match 71.7%; Score 33; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 8.9e+04;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VRIGHLYIL 9
| | | | |
Db 1 VPISHLYIL 9

RESULT 4
US-09-017-743C-31
; Sequence 31, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; Sidney, John
; Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>


```
RESULT 8
US-09-909-460-51
; Sequence 51, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-460-51

Query Match      63.0%; Score 29; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IGHLY 7
Db 5 IGHLY 9

RESULT 9
US-09-812-528-3
; Sequence 3, Application US/09812528
; Patent No. US20010018210A1
; GENERAL INFORMATION:
; APPLICANT: Bachovchin, William
; APPLICANT: Wallner, Barbara
; TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
; VITRO
; FILE REFERENCE: 10248/7015
; CURRENT APPLICATION NUMBER: US/09/812,528
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/060,306
; PRIOR FILING DATE: 1997-09-29
; PRIOR APPLICATION NUMBER: US 09/162,934
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-812-528-3

Query Match      63.0%; Score 29; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IGHLY 7
Db 5 IGHLY 9

RESULT 10
US-09-847-185-23
; Sequence 23, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; APPLICANT: Martelange, Val'rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/923,831
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-6

Query Match      63.0%; Score 29; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IGHLY 7
Db 5 IGHLY 9

RESULT 11
US-09-923-831-6
; Sequence 6, Application US/09923831
; Patent No. US20020115142A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Val'rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/923,831
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-6

Query Match      63.0%; Score 29; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IGHLY 7
Db 5 IGHLY 9

TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
RESPONSE USING SAME

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/847,185
FILING DATE: 01-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/201,931
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-847-185-23

Query Match      63.0%; Score 29; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IGHLY 7
Db 5 IGHLY 9
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QY 3 IGHLY 7
Db 5 IGHLY 9

RESULT 12
US-09-017-743C-32
; Sequence 32, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; Sidney, John
; Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-017-743C-32

Query Match 60.9%; Score 28; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 8.9e+04;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VRIGHLYL 9
Db 1 VPISHLYAL 9

RESULT 13
US-09-766-889A-7
; Sequence 7, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin

; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-7

Query Match 56.5%; Score 26; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 8.9e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 GHLYIL 9
Db 4 GHSYVL 9

RESULT 14
US-10-026-001-3
; Sequence 3, Application US/10026001
; Patent No. US20020122791A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: ANTIGENIC CR-18 COMPOUNDS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS AND METHODS FOR USING SAME
; FILE REFERENCE: G2 210800
; CURRENT APPLICATION NUMBER: US/10/026,001
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,820
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-001-3

Query Match 56.5%; Score 26; DB 12; Length 9;
Best Local Similarity 60.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 GHLYI 8
Db 5 GHMYV 9

RESULT 15
US-09-894-018-319
; Sequence 319, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denisw
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; MINIGENES AND PEPTIDES THEREBY
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
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; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 319
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Transgenic mouse
US-09-894-018-319

Query Match      52.2%; Score 24; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 8.9e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 VRIGHL 6
       : ||||
Db      1 IMIGHL 6
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Search completed: December 19, 2002, 16:49:34
Job time : 25 secs

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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:42:33 : Search time 14 Seconds
(without alignments)
18.915 Million cell updates/sec

Title: US-09-692-401-4
Perfect score: 46
Sequence: 1 VRIGHLYIL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 66399

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2.6/ptodata/1/1aa/5B-COMB.pep:*
3: /cgn2.6/ptodata/1/1aa/6A-COMB.pep:*
4: /cgn2.6/ptodata/1/1aa/6B-COMB.pep:*
5: /cgn2.6/ptodata/1/1aa/PCTUS-COMB.pep:*
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query			Description
		Match	Length	ID	
1	38	82.6	9	1	US-07-938-334C-3
2	38	82.6	9	1	US-08-073-103A-16
3	38	82.6	9	1	US-08-443-341-16
4	38	82.6	9	2	US-08-498-461-15
5	38	82.6	9	3	US-08-354-679C-16
6	38	82.6	9	4	US-08-393-273E-16
7	38	82.6	9	4	US-08-443-580F-16
8	31	67.4	9	1	US-08-217-188A-27
9	31	67.4	9	1	US-08-687-226-27
10	31	67.4	9	3	US-08-667-725B-27
11	31	67.4	9	4	US-09-007-748-27
12	29	63.0	9	1	US-07-938-334C-4
13	29	63.0	9	1	US-08-073-103A-17
14	29	63.0	9	1	US-08-186-266-2
15	29	63.0	9	1	US-08-186-266-11
16	29	63.0	9	1	US-08-186-266-11
17	29	63.0	9	1	US-08-443-341-17
18	29	63.0	9	1	US-08-787-547-51
19	29	63.0	9	2	US-08-498-461-11
20	29	63.0	9	2	US-08-902-516-23
21	29	63.0	9	2	US-09-036-582-3
22	29	63.0	9	3	US-08-880-963-18
23	29	63.0	9	3	US-08-354-679C-17
24	29	63.0	9	4	US-08-159-339A-576
25	29	63.0	9	4	US-09-183-931-27
26	29	63.0	9	4	US-09-183-931-33
27	29	63.0	9	4	US-09-183-273E-17
					Sequence 6, Appli

28	29	63.0	9	4	US-09-162-934-3	Sequence 3, Appli
29	29	63.0	9	4	US-09-061-388-18	Sequence 18, Appl
30	29	63.0	9	4	US-09-166-448-47	Sequence 47, Appl
31	29	63.0	9	4	US-09-567-995-6	Sequence 6, Appli
32	29	63.0	9	4	US-09-099-543C-18	Sequence 18, Appl
33	29	63.0	9	4	US-09-412-928-18	Sequence 18, Appl
34	29	63.0	9	4	US-08-443-580F-17	Sequence 17, Appl
35	29	63.0	9	4	US-09-461-083-18	Sequence 18, Appl
36	29	63.0	9	4	US-09-705-160-27	Sequence 27, Appl
37	29	63.0	9	4	US-09-705-160-33	Sequence 33, Appl
38	29	63.0	9	4	US-09-165-863-3	Sequence 3, Appli
39	29	63.0	9	4	US-09-697-884-47	Sequence 47, Appl
40	29	63.0	9	5	PCT-US95-04975-1	Sequence 1, Appli
41	27	58.7	9	1	US-08-217-188A-28	Sequence 28, Appl
42	27	58.7	9	1	US-08-687-226-28	Sequence 28, Appl
43	27	58.7	9	3	US-08-667-725B-28	Sequence 28, Appl
44	27	58.7	9	4	US-09-007-748-28	Sequence 28, Appl
45	26	56.5	9	1	US-07-938-334C-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-07-938-334C-3
: Sequence 3, Application US/07938334C
: Patent No. 5405940
: GENERAL INFORMATION:
: APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
: APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
: TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
: TITLE OF INVENTION: MAGE GENES AND USES THEREOF
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Felfe & Lynch
: STREET: 805 Third Avenue
: CITY: New York City
: STATE: New York
: COUNTRY: USA
: ZIP: 10022
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/938,334C
: FILING DATE: 31-AUG-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Hanson, No. 5405940man D.
: REGISTRATION NUMBER: 30,946
: REFERENCE/DOCKET NUMBER: LUD 293
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 688-9200
: TELEFAX: (212) 838-3884
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acid residues
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: MAGE-21 derived nonapeptide
US-07-938-334C-3

Query Match 82.6% Score 38 DB 1 Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VRIGHLY 7
Db 3 VRIGHLY 9
|||||

```
RESULT 2
US-08-073-103A-16
; Sequence 16, Application US/08073103A
; Patent No. 5462871
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: De Plaen, Etienne
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Gaugler, Beatrice
; APPLICANT: Van den Eynde, Benoit
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,103A
; FILING DATE: 31-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5462871man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-073-103A-16

Query Match 82.6%; Score 38; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
Db 3 VRIGHLY 9

RESULT 3
US-08-443-341-16
; Sequence 16, Application US/08443341
; Patent No. 5695994
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: De Plaen, Etienne
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Gaugler, Beatrice
; APPLICANT: Van den Eynde, Benoit
```

```
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,341
; FILING DATE: 17-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,103
; FILING DATE: 7-JUNE-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5695994man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-443-341-16

Query Match 82.6%; Score 38; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
Db 3 VRIGHLY 9

RESULT 4
US-08-498-461-15
; Sequence 15, Application US/08498461
; Patent No. 5827073
; GENERAL INFORMATION:
; APPLICANT: Luescher, Immanuel; Anjuere, Fabienne;
; APPLICANT: Layer, Andreas; Romero, Pedro; Cerottini, Jean-Charles
; TITLE OF INVENTION: Photoreactive Peptide Derivatives
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/498,461
;; FILING DATE: 5-JULY-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 5827073man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5403
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
US-08-498-461-15

Query Match 82.6%; Score 38; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
| | | | |
Db 3 VRIGHLY 9

RESULT 5
US-08-354-679C-16
; Sequence 16, Application US/08354679C
; Patent No. 6034214
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
; APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,679C
; FILING DATE: 13-DECEMBER-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAER, MADELINE F.
; REGISTRATION NUMBER: 36,437
; REFERENCE/DOCKET NUMBER: LUD 5293.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-354-679C-16

Query Match 82.6%; Score 38; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
| | | | |
Db 3 VRIGHLY 9

RESULT 6
US-08-393-273E-16
; Sequence 16, Application US/08393273E
; Patent No. 6222012
; GENERAL INFORMATION:
; APPLICANT: BOON-FALLEUR, Thierry; VAN DER BRUGGEN,
; APPLICANT: PLAEN, Etienne; LORQUIN, Christophe; TRAVERSARI, Catia;
; APPLICANT: GAUGLER, Beatrice; VAN DEN EYNDE, Benoît; ROMERO, Pedro
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,273E
; FILING DATE: 23-February-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,103
; FILING DATE: 7-June-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-August-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/037,230
; FILING DATE: 26-March-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6222012man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-273E-16

Query Match 82.6%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
| | | | |
Db 3 VRIGHLY 9

RESULT 7
US-08-443-580F-16
; Sequence 16, Application US/08443580F
; Patent No. 6379901

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; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; Gaugler, Beatrice; Van den Eynde, Benoit
; TITLE OF INVENTION: Method For Screening For Cancer
; Using Binders For MAGE Related Peptides And Complexes
; Of The Peptide And HLA Molecules
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM, PH.D./2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,580F
; FILING DATE: 17-May-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,103
; FILING DATE: 7-JUNE-1993
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUGUST-1992
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6379901man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-443-580F-16

Query Match 82.6%; Score 38; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRIGHLY 7
DB 3 VRIGHLY 9

RESULT 8
US-08-217-188A-27
; Sequence 27, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-443-580F-17

Query Match 67.4%; Score 31; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 IGHLYIL 9
DB 2 ISHLYIL 8

RESULT 9
US-08-687-226-27
; Sequence 27, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
;
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-188A-27
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; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-188A-27
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Query Match 67.4%; Score 31; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 IGHLYIL 9
DB 2 ISHLYIL 8
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RESULT 9
US-08-687-226-27
; Sequence 27, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: MAGE-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
;
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-217-188A-27
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TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acid residues
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-687-226-27

Query Match 67.4%; Score 31; DB 1; Length 9;
 Best Local Similarity 85.7%; Pred. No. 1.9e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 IGHLYIL 9
 1 | | | | |
 Db 2 ISHLVIL 8

RESULT 10

US-08-667-725B-27
 Sequence 27, Application US/08667725B
 Patent No. 6063900
 GENERAL INFORMATION:
 APPLICANT: Melief, Cornelis J. M.
 APPLICANT: Visseren, M. J. W.
 APPLICANT: Kast, W. M.
 APPLICANT: van der Bruggen, Pierre
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: Isolated Tumor Rejection Antigen
 TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski LLP
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/667,725B
 FILING DATE: 21 June 1996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6063900man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3000
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acid residues
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-667-725B-27

Query Match 67.4%; Score 31; DB 3; Length 9;
 Best Local Similarity 85.7%; Pred. No. 1.9e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 IGHLYIL 9
 1 | | | | |
 Db 2 ISHLVIL 8

RESULT 11

US-09-007-748-27
 Sequence 27, Application US/09007748
 Patent No. 6147187
 GENERAL INFORMATION:
 APPLICANT: Melief, Cornelis J. M.
 APPLICANT: Visseren, M. J. W.
 APPLICANT: Kast, W. M.
 APPLICANT: van der Bruggen, Pierre
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: Isolated Tumor Rejection Antigen
 TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski LLP
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/007,748
 FILING DATE: 15 January 1998
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6147187man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3000
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acid residues
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-007-748-27

Query Match 67.4%; Score 31; DB 4; Length 9;
 Best Local Similarity 85.7%; Pred. No. 1.9e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 IGHLYIL 9
 1 | | | | |
 Db 2 ISHLVIL 8

RESULT 12

US-07-938-334C-4
 Sequence 4, Application US/07938334C
 Patent No. 5405940
 GENERAL INFORMATION:
 APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
 APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
 TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
 TITLE OF INVENTION: MAGE GENES AND USES THEREOF
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/938,334C
; FILING DATE: 31-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 540594 Oman D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: MAGE-3 derived nonapeptide
; US-07-938-334C-4

Query Match 63.0%; Score 29; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGHLY 7
Db 5 IGHLY 9

RESULT 13
US-08-073-103A-17
; Sequence 17, Application US/08073103A
; Patent No. 5462871
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: De plaen, Etienne
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Gaugler, Beatrice
; APPLICANT: Van den Eynde, Benoit
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Feife & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,103A
; FILING DATE: 7-JUNE-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5462871man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 838-3884
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 17:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-073-103A-17

Query Match 63.0%; Score 29; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGHLY 7
Db 5 IGHLY 9

RESULT 14
US-08-186-266-2
; Sequence 2, Application US/08186266
; Patent No. 5662907
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
; TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
; TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,266
; FILING DATE: 25-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
; FILING DATE: 29-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-186-266-2

Query Match 63.0%; Score 29; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: December 19, 2002, 16:46:00
Job time : 15 secs

QY 3 IGHLY 7
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Db 5 IGHLY 9

RESULT 15
US-08-186-266-11
; Sequence 11, Application US/08186266
; Patent No. 5662907
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
; TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
; TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,266
; FILING DATE: 25-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
; FILING DATE: 29-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-186-266-11

Query Match 63.0%; Score 29; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 IGHLY 7
|||||
Db 5 IGHLY 9

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:45:43 ; Search time 34 Seconds
(without alignments)
39.191 Million cell updates/sec

Title: US-09-692-401-5
Perfect score: 50
Sequence: 1 VVRIGHLVIL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 174064

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	10	AAE02083	MAGE-A12 human leu
2	46	92.0	9	AAE12995	Human MAGE-12 T-ce
3	46	92.0	9	AAE02082	MAGE-A12 human leu
4	42	84.0	8	AAE02084	MAGE-A12 human leu
5	42	84.0	9	AAE02083	MAGE-21 nonapeptid
6	42	84.0	9	AAE02083	MAGE-21 nonapeptid
7	42	84.0	9	AAE02081	Immunogenic peptid
8	42	84.0	9	AAE02081	MAGE-A12 human leu
9	42	84.0	10	AAE23043	MAGE-12/HUA-B44 tu
10	37	74.0	10	AAE47343	Immunogenic peptid

11	35	70.0	9	22	AAG84743	MAGE3 HLA-B7 super
12	35	70.0	9	22	AAE76152	Tumour associated
13	33	66.0	9	18	AAW45704	MAGE-2 170 peptide
14	33	66.0	9	20	AAE46232	Immunogenic peptid
15	33	66.0	9	20	AAE46263	Immunogenic peptid
16	33	66.0	9	20	AAE47310	Immunogenic peptid
17	33	66.0	9	20	AAE47329	Immunogenic peptid
18	33	66.0	9	20	AAE47944	Immunogenic peptid
19	33	66.0	9	20	AAE47950	Immunogenic peptid
20	33	66.0	9	22	AAE48191	Immunogenic peptid
21	33	66.0	9	22	AAE06856	Human MAGE-A3 pept
22	33	66.0	9	22	AAE84718	MAGE2 HLA-B7 super
23	33	66.0	9	23	ABJ00115	MAGE2 170 protein
24	33	66.0	9	23	ABJ00152	MAGE2/3 derived HL
25	33	66.0	10	20	AAE46214	Immunogenic peptid
26	33	66.0	10	20	AAE46283	Immunogenic peptid
27	33	66.0	10	20	AAE46333	Immunogenic peptid
28	33	66.0	10	20	AAE47342	Immunogenic peptid
29	33	66.0	10	20	AAE47356	Immunogenic peptid
30	33	66.0	10	20	AAE47357	Immunogenic peptid
31	33	66.0	10	20	AAE47977	Immunogenic peptid
32	33	66.0	10	20	AAE48011	Immunogenic peptid
33	33	66.0	10	22	AAG84722	MAGE2 HLA-B7 super
34	33	66.0	10	22	AAG84723	MAGE2 HLA-B7 super
35	33	66.0	10	22	AAG84744	MAGE3 HLA-B7 super
36	33	66.0	10	22	AAG84745	MAGE3 HLA-B7 super
37	33	66.0	10	22	AAE76197	Tumour associated
38	33	66.0	10	22	AAE76198	Tumour associated
39	33	66.0	10	23	ABJ00200	MAGE2 derived HLA
40	31	62.0	9	16	AAE80904	MAGE-2 peptide (re
41	31	62.0	9	18	AAW45705	MAGE-2 170 peptide
42	31	62.0	9	18	AAW45707	MAGE-2 170 peptide
43	31	62.0	9	18	AAW46555	MAGE-2 peptide (re
44	31	62.0	9	20	AAE45987	Immunogenic peptid
45	31	62.0	9	20	AAE46404	Immunogenic peptid

ALIGNMENTS

RESULT 1
AAE02083
ID AAE02083 standard; peptide; 10 AA.
AC
AAE02083;
XX
DT 31-JUL-2001 (first entry)
XX
DE MAGE-A12 human leukocyte antigen-binding peptide #3.

XX Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
XX CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
XX brain tumour; sarcoma; vaccine; gene therapy.

OS Homo sapiens.

XX WO200129220-A2.

PN 26-APR-2001.

XX 19-OCT-2000; 2000WO-US28852.

XX 19-OCT-1999; 99US-0160374.

XX 01-FEB-2000; 2000US-0179570.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;

XX WPI; 2001-328498/34.

XX New antigenic peptides derived from MAGE-A12 polypeptides, useful for
PT diagnosis and treatment of cancer, such as bladder, lung, breast,

PT brain, prostate and renal carcinomas -
PS claim 2; Page 42; 69pp; English.
XX
CC The patent discloses antigenic peptides derived from MAGE-A12
CC protein and presented by human leukocyte antigens (HLAs). These
CC antigenic peptides when presented by an antigen presenting cell
CC having a HLA class I molecule, effectively induce the activation
CC and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is
CC useful for treating a subject having a disorder characterised by
CC expression of MAGE-A12. The protein microarray comprising MAGE-A12
CC is useful for diagnosing a disorder, especially cancer, by determining
CC the binding of an antibody, T lymphocytes or a HLA molecule isolated
CC from the subject suspected of having the disorder characterised by the
CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,
CC including bladder carcinomas, melanomas, oesophageal, lung, head and
CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
CC prostate and renal carcinomas and to produce antibodies. MAGE-A12
CC antibodies are useful for diagnosing disorders characterised by
CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-12 peptides
CC are used as vaccines. They are also used in gene therapy.
CC The present sequence is MAGE-A12 HLA class-I-binding peptide. This
CC antigenic peptide is presented by major histocompatibility complex
CC (MHC) and is recognised by CTLs.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 50; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00086;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVRIGHLYIL 10
| | | | | | | | | |
DB 1 VVRIGHLYIL 10
| | | | | | | | | |
RESULT 2
AAE12995
ID AAE12995 standard; peptide; 9 AA.
AC AAE12995;
XX
XX 28-JAN-2002 (first entry)
XX
XX Human MAGE-12 T-cell epitope.
XX
XX Human; MAGE-12; immunostimulant; gene therapy; cytostatic; immunotherapy;
KW vaccine; melanoma; T-cell epitope; tumour rejection antigen; cancer.
XX
XX Homo sapiens.
XX
XX WO200174847-A2.
XX
XX 11-OCT-2001.
XX
XX 29-MAR-2001; 2001WO-US10312.
XX
XX 30-MAR-2000; 2000US-193206P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Panelli M, Bettinotti M, Marincola F;
XX WPI; 2001-662964/76.
XX N-PSDB; AAD21284.
XX
XX Novel T cell epitope of MAGE-12 is a tumor rejection antigen for a
PT melanoma expressing HLA-Cw0702 recognized by tumor-infiltrating
PT lymphocytes and useful to treat cancer particularly melanoma -
XX
XX Claim 1; Page 14; 17pp; English.
PS
XX The invention relates to an isolated and purified T cell epitope of

CC MAGE-12. MAGE-12 is a tumour rejection antigen for melanoma which
CC expresses MHC-class I molecule HLA-Cw0702 recognised by tumour-
CC infiltrating lymphocytes. The epitope or a vector encoding the epitope
CC is used to treat cancer, particularly melanoma expressing HLA-Cw
CC asterisk 0702. The epitope has widespread utility in cancer immunotherapy
CC since MAGE-12 is mostly found in tumours. The present sequence is
CC human MAGE-12 T-cell epitope.
XX
SQ Sequence 9 AA;
Query Match 92.0%; Score 46; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VRIGHLYIL 10
| | | | | | | | | |
DB 1 VRIGHLYIL 9
| | | | | | | | | |
RESULT 3
AAE02082
ID AAE02082 standard; peptide; 9 AA.
XX
AC AAE02082;
XX
XX 31-JUL-2001 (first entry)
XX
XX MAGE-A12 human leukocyte antigen-binding peptide #2.
XX
XX Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
KW brain tumour; sarcoma; vaccine; gene therapy.
XX
XX Homo sapiens.
XX
XX WO200129220-A2.
XX
XX 26-APR-2001.
XX
XX 19-OCT-2000; 2000WO-US28852.
XX
XX 19-OCT-1999; 99US-0160374.
XX
XX 01-FEB-2000; 2000US-0179570.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;
XX WPI; 2001-328498/34.
XX
XX New antigenic peptides derived from MAGE-A12 polypeptides, useful for
PT diagnosis and treatment of cancer, such as bladder, lung, breast,
PT brain, prostate and renal carcinomas -
XX
XX Claim 2; Page 42; 69pp; English.
XX
XX The patent discloses antigenic peptides derived from MAGE-A12
CC protein and presented by human leukocyte antigens (HLAs). These
CC antigenic peptides when presented by an antigen presenting cell
CC having a HLA class I molecule, effectively induce the activation
CC and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is
CC useful for treating a subject having a disorder characterised by
CC expression of MAGE-A12. The protein microarray comprising MAGE-A12
CC is useful for diagnosing a disorder, especially cancer, by determining
CC the binding of an antibody, T lymphocytes or a HLA molecule isolated
CC from the subject suspected of having the disorder characterised by the
CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,
CC including bladder carcinomas, melanomas, oesophageal, lung, head and
CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
CC prostate and renal carcinomas and to produce antibodies. MAGE-A12
CC antibodies are useful for diagnosing disorders characterised by
CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-12 peptides
CC are used as vaccines. They are also used in gene therapy.

CC The present sequence is MAGE-A12 HLA class-I-binding peptide. This
CC antigenic peptide is presented by major histocompatibility complex
CC (MHC) and is recognised by CTLs.

XX SQ Sequence 9 AA;

Query Match 92.0%; Score 46; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VRIGHLYIL 10
| | | | | | | |
Db 1 VRIGHLYIL 9

RESULT 4
AAE02084
ID AAE02084 standard; peptide; 8 AA.

XX AC AAE02084;

XX DT 31-JUL-2001 (first entry)

XX DE MAGE-A12 human leukocyte antigen-binding peptide #4.

XX KW Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
KW brain tumour; sarcoma; vaccine; gene therapy.

XX OS Homo sapiens.

XX PN WO200129220-A2.

XX PD 26-APR-2001.

XX PF 19-OCT-2000; 2000WO-US28852.

XX PR 19-OCT-1999; 99US-0160374.

XX PR 01-FEB-2000; 2000US-0179570.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;

XX DR WPI; 2001-328498/34.

XX PT New antigenic peptides derived from MAGE-A12 polypeptides, useful for
PT diagnosis and treatment of cancer, such as bladder, lung, breast,
PT brain, prostate and renal carcinomas

XX PS Claim 1; Page 43; 69pp; English.

XX CC The patent discloses antigenic peptides derived from MAGE-A12
CC protein and presented by human leukocyte antigens (HLAs). These
CC antigenic peptides when presented by an antigen presenting cell
CC having a HLA class I molecule, effectively induce the activation
CC and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is
CC useful for treating a subject having a disorder characterised by
CC expression of MAGE-A12. The protein microarray comprising MAGE-A12
CC is useful for diagnosing a disorder, especially cancer, by determining
CC the binding of an antibody, T lymphocytes or a HLA molecule isolated
CC from the subject suspected of having the disorder characterised by the
CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,
CC including bladder carcinomas, melanomas, oesophageal, lung, head and
CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
CC prostate and renal carcinomas and to produce antibodies. MAGE-A12
CC antibodies are useful for diagnosing disorders characterised by
CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-12 peptides
CC are used as vaccines. They are also used in gene therapy.
CC The present sequence is MAGE-A12 HLA class-I-binding peptide. This
CC antigenic peptide is presented by major histocompatibility complex
CC (MHC) and is recognised by CTLs.

SQ Sequence 8 AA;

Query Match 84.0%; Score 42; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RIGHLYIL 10
| | | | | | | |
Db 1 RIGHLYIL 8

RESULT 5
AAR50283
ID AAR50283 standard; Protein; 9 AA.

XX AC AAR50283;

XX DT 26-SEP-1994 (first entry)

XX DE MAGE-21 nonapeptide.

XX KW MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;
KW histocompatibility; human leucocyte antigen; probe; treatment;
KW therapy; vaccine.

XX OS Synthetic.

XX PN WO9405304-A.

XX PD 17-MAR-1994.

XX PF 30-AUG-1993; 93WO-US08157.

XX PR 31-AUG-1992; 92US-0938334.

XX PR 26-MAR-1993; 93US-0037230.

XX PR 07-JUN-1993; 93US-0073103.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Boon-falleur T, De Plaen E, Lurquin C, Traversari C;
PI Van Derbruggen P;

XX DR WPI; 1994-100844/12.

XX DR N-PSDB; AAQ44753.

XX PT New nona-peptide derived from tumour rejection antigen precursor
PT - presented by HLA-A1 cancer cells, for use in diagnosis or
PT therapy of esp. melanoma and breast cancer.

XX PS Disclosure; Page 20; 33pp; English.

XX CC An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-
CC Pro-Ile-Gly-His-Leu-Tyr is derived from the tumour rejection antigen
CC precursor encoded by the MAGE-3 gene and presented by HLA-A1. The
CC nonapeptide can be used in a vaccine to treat a cancerous condition
CC involving HLA-A1 subtype cancerous cells. The nucleic acid encoding
CC the nonapeptide can be used as a probe to identify tumour cells.
CC This sequence is homologous to the peptide described and is encoded
CC by the MAGE-21 gene.

XX SQ Sequence 9 AA;

Query Match 84.0%; Score 42; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVRIGHLY 8
| | | | | | | |

Db 2 VVRIGHLY 9
| | | | | | | |

RESULT 6
AAR99345

ID AAR99345 standard; Protein; 9 AA.
 AC AAR99345;
 XX
 DT 22-APR-1997 (first entry)
 XX
 DE MAGE-21 nonapeptide.
 XX
 KW HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human;
 KW tumour rejection antigen precursor; TRA: MAGE-1; tumour; cancer cell;
 KW antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
 KW therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9626214-A1.
 XX
 PD 29-AUG-1996.
 XX
 PF 01-FEB-1996; 96WO-US01489.
 XX
 PR 23-FEB-1995; 95US-0393273.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Boon-Falleur T, De Plaen E, Gaugler B, Lurquin C;
 PI Romero P, Traversari C, Van Den Eynde B, Van Der Bruggen P;
 XX
 DR WPI; 1996-402317/40.
 DR N-PSDB; AAT35410.
 XX
 PT New nona:peptide(s) that bind to HLA molecule(s) and induce lysis -
 PT by specific cytolytic T cells, for diagnosis and treatment of
 PT tumours and to expand T cells in vitro.
 XX
 PS Example 4; Fig 4; 41pp; English.
 XX
 CC AAR99343-R99350 represent MAGE nonapeptides, based on the tumour
 CC rejection antigen region of the full length MAGE sequences. These
 CC peptides were used to design the nonapeptides of the invention (see
 CC AAR99337-R99342), which bind to a HLA molecule on a cell, and provoke
 CC lysis by cytolytic T cells (CTLs) specific for a complex of the HLA
 CC molecule and nonapeptide. The nonapeptides can be used diagnostically to
 CC identify tumours expressing a particular HLA molecule, or to identify
 CC cancer cells. The peptides can also be used therapeutically, to induce a
 CC CTL response to tumours (where the peptides are optionally coupled to
 CC tumour-specific antibodies), or to induce a response by CTLs that are
 CC otherwise inactive. The peptide sequences may also be used to expand
 CC specific CTLs in vitro for later return to the patient, such as for
 CC treating melanoma. Tumour cells can be identified by using DNA encoding
 CC the nonapeptides as probes. Non-human cells transformed with the HLA-A1
 CC gene and a DNA sequence encoding one of the peptides, can be used to
 CC generate CTLs, or to detect the presence of CTLs in human samples. The
 CC non-human transformed cells, when polytransformed, are universal effector
 CC cells, and can be used in vaccines, or for treating melanoma or breast
 CC cancer.
 XX
 SQ Sequence 9 AA;
 Query Match 84.0%; Score 42; DB 17; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVRIGHLY 8
 Db |||||
 2 VVRIGHLY 9
 RESULT 7
 AAY46062
 ID AAY46062 standard; Peptide; 9 AA.
 XX
 AC AAY46062;
 4

XX 01-DEC-1999 (first entry)
 XX Immunogenic peptide having a human leukocyte antigen binding motif #673.
 DE
 XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98WO-US05039.
 XX
 PR 13-MAR-1998; 98WO-US05039.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Cellis E, Grey HM, Southwood S;
 PI WPI; 1999-551214/46.
 DR
 DR New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 PT
 PS Claim 1; Page 54; 150pp; English.
 XX
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 XX
 SQ Sequence 9 AA;
 Query Match 84.0%; Score 42; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVRIGHLY 8
 Db |||||
 2 VVRIGHLY 9
 RESULT 8
 AAE02081
 ID AAE02081 standard; peptide; 9 AA.
 XX
 AC AAE02081;
 XX
 DT 31-JUL-2001 (first entry)

XX DE MAGE-A12 human leukocyte antigen-binding peptide #1.
 XX KW Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
 KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
 KW brain tumour; sarcoma; vaccine; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200129220-A2.
 XX PD 26-APR-2001.
 XX PF 19-OCT-2000; 2000WO-US28852.
 XX PR 19-OCT-1999; 99US-0160374.
 XX PR 01-FEB-2000; 2000US-0179570.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;
 XX DR WPI; 2001-328498/34.
 XX PT New antigenic peptides derived from MAGE-A12 polypeptides, useful for
 PT diagnosis and treatment of cancer, such as bladder, lung, breast,
 PT brain, prostate and renal carcinomas.
 XX PS Example 1; Page 42; 69pp; English.
 XX CC The patent discloses antigenic peptides derived from MAGE-A12
 CC protein and presented by human leukocyte antigens (HLAs). These
 CC antigenic peptides when presented by an antigen presenting cell
 CC having a HLA class I molecule, effectively induce the activation
 CC and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is
 CC useful for treating a subject having a disorder characterised by
 CC expression of MAGE-A12. The protein microarray comprising MAGE-A12
 CC is useful for diagnosing a disorder, especially cancer, by determining
 CC the binding of an antibody, T lymphocytes or a HLA molecule isolated
 CC from the subject suspected of having the disorder characterised by the
 CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers,
 CC including bladder carcinomas, melanomas, oesophageal, lung, head and
 CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
 CC prostate and renal carcinomas and to produce antibodies. MAGE-A12
 CC antibodies are useful for diagnosing disorders characterised by
 CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-A12 peptides
 CC are used as vaccines. They are also used in gene therapy.
 CC The present sequence is MAGE-A12 HLA class-I-binding peptide. This
 CC antigenic peptide is presented by major histocompatibility complex
 CC (MHC) and is recognised by CTLs.
 XX SQ Sequence 9 AA;
 Query Match 84.0%; Score 42; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVRIGHLY 8
 | | | | | | | |
 Db 2 VVRIGHLY 9
 RESULT 9
 AAW23043
 ID AAW23043 standard; Peptide; 10 AA.
 XX AC AAW23043;
 XX DT 25-FEB-1998 (first entry)
 XX DE MAGE-12/HLA-B44 tumour rejection antigen.
 XX KW MAGE-12; tumour rejection antigen precursor; TRAP; HLA-B44;

KW human leukocyte antigen B44; cytotoxic T lymphocyte; cancer;
 KW melanoma; therapy; diagnosis; vaccine.
 XX OS Homo sapiens.
 XX PN WO9731017-A1.
 XX PD 28-AUG-1997.
 XX PF 05-FEB-1997; 97WO-US01915.
 XX PR 20-FEB-1996; 96US-0602506.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Boon-Falleur T, Coullie P, Herman J, Luescher I;
 XX PI Van Der Bruggen P;
 XX DR WPI; 1997-435086/40.
 XX PT Tumour rejection antigens presented by human leukocyte antigen B44
 PT molecules - useful to identify HLA-B44 positive cells for diagnosis
 PT and therapy of cellular abnormalities
 XX PS Claim 2; Page 51; 74pp; English.
 XX CC This peptide is a tumour rejection antigen presented by a HLA-B44
 CC molecule and derived from a MAGE-12 tumour rejection antigen
 CC precursor (TRAP). Claimed tumour rejection antigens (AAW23038-43)
 CC are able to bind to HLA-B44 positive cells, making them useful in
 CC identifying cells which present HLA-B44 molecules on their
 CC surfaces for use in the diagnosis and therapy of cellular
 CC abnormalities. The complex of the tumour rejection antigen and HLA
 CC molecule provokes a cytolytic T cell response. The tumour
 CC rejection antigens, or complexes of tumour rejection antigens and
 CC HLA-B44, can be used as vaccines to treat disorders characterised
 CC by expression of the TRAP molecule such as cancer, especially
 CC melanoma. Vaccines can also be prepared from cells which present
 CC the tumour rejection antigen/HLA complexes on their surface, such
 CC as non-proliferative cancer cells and non-proliferative
 CC transfectants.
 XX SQ Sequence 10 AA;
 Query Match 84.0%; Score 42; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VVRIGHLY 8
 | | | | | | | |
 Db 3 VVRIGHLY 10
 RESULT 10
 AAY47343
 ID AAY47343 standard; Peptide; 10 AA.
 XX AC AAY47343;
 XX DT 01-DEC-1999 (first entry)
 XX DE Immunogenic peptide having a human leukocyte antigen binding motif #1954.
 XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9945954-A1.

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XX PD 16-SEP-1999.
XX PF 13-MAR-1998; 98WO-US05039.
XX PR 13-MAR-1998; 98WO-US05039.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -
XX Claim 1; Page 104; 150pp; English.
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX having a human major histocompatibility complex (MHC) Class I (also
XX known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX response against the antigen from which the peptide is derived.
XX Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX normally induced by an antigen in the form of a peptide fragment bound
XX to a HLA molecule, rather than the intact foreign antigen itself, and
XX are particularly important in tumour rejection and in fighting viral
XX infections. The peptides are therefore useful therapeutically to treat
XX or prevent viral infections and cancers in mammals (especially humans)
XX e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX They can be administered as vaccines to elicit an immune response in
XX individuals susceptible or otherwise at risk of viral infection or
XX cancer, or used to treat chronic or acute conditions. They are also
XX useful diagnostically, and can be used to induce a cytotoxic T cell
XX response, by contacting a cytotoxic T cell with the peptide e.g. to
XX produce CTLs ex vivo for infusion back into a patient. The
XX polynucleotides encoding the immunogenic peptides are also useful
XX therapeutically and for immunisation as above.
XX Sequence 10 AA;
SQ Query Match 74.0%; Score 37; DB 20; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVRIGHLYIL 10
II I IIIII
Db 1 VVPISHLYIL 10

RESULT 11
AAG84743
ID AAG84743 standard; Peptide; 9 AA.
AC AAG84743;
XX 10-SEP-2001 (first entry)
XX MAGE3 HLA-B7 supermotif-bearing peptide #9.
XX Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte;
XX CTL; MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine;
XX cancer; cytostatic; immunostimulant.
XX Homo sapiens.
XX Synthetic.
XX WO200142267-A1.
XX 14-JUN-2001.
XX 11-DEC-2000; 2000WO-US33545.

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XX 10-DEC-1999; 99US-0458298.
XX (EPIM-) EPIMMUNE INC.
XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
XX Keogh E;
XX WPI; 2001-375002/39.
XX An isolated prepared MAGE2/3 epitope (I) for use in pharmaceuticals for
XX the treatment and prevention of cancer -
XX Claim 1; Page 156; 171pp; English.
XX The present invention describes MAGE2/3 epitopes (I). Also described
XX are: (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo
XX and binds to a complex of (1); (2) a peptide (II) comprising (1) and a
XX second epitope and has less than 50 contiguous amino acids; (3) a vaccine
XX composition comprising (II), a unit dose of a peptide with at least 50
XX contiguous amino acids with 100% identity to the native peptide sequence
XX of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
XX encoding (1); and (5) an isolated nucleic acid encoding (II). (1) has
XX cytostatic activity, and can be used in vaccines and as an
XX immunostimulant. A vaccine of (3) is useful for the treatment and
XX prevention of cancer. (1) is useful for monitoring or evaluating an
XX immune response by incubating a T-lymphocyte sample from a patient with
XX (1) that binds to an human leukocyte antigen (HLA) allele present in the
XX patient and detecting the presence of the T-lymphocyte that binds to the
XX peptide. The vaccine allows the opportunity to combine epitopes derived
XX from multiple tumour-associated molecules reducing the likelihood of
XX tumour escape due to antigen loss. AAG84515 to AAG84909 and AAG99725
XX represent amino acid sequences used in the exemplification of the
XX present invention.
XX Sequence 9 AA;
SQ Query Match 70.0%; Score 35; DB 22; Length 9;
Best Local Similarity 85.7%; Pred. No. 7.8e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLYIL 10
IIIIII
Db 3 IGHLYII 9

RESULT 12
AAB76152
ID AAB76152 standard; Peptide; 9 AA.
XX AAB76152;
XX 10-APR-2001 (first entry)
XX Tumour associated antigen MAGE3 immunogenic peptide.
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
XX cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
XX HLA binding peptide; immune response; glycoprotein; cytostatic;
XX virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
XX human immunodeficiency virus; protozoicide; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
XX cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
XX renal carcinoma; cervical carcinoma; lymphoma; malaria;
XX condyloma acuminatum.
XX Homo sapiens.
XX WO200100225-A1.
XX 04-JAN-2001.
XX 28-JUN-2000; 2000WO-US17842.

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XX 29-JUN-1999; 99US-0141422.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Sidney J, Southwood S;
XX WPI; 2001-112389/12.
XX Composition comprising human leukocyte antigen binding peptide which
XX comprises isolated, prepared epitope useful for treating viral
XX infections such as acquired immunodeficiency syndrome, and cancer -
XX Claim 1; Page 48; 58pp; English.
XX The present invention describes a composition (I) which comprises at
XX least one human leukocyte antigen (HLA) binding peptide comprising an
XX isolated, prepared epitope comprising one of 547 8-11 residue amino acid
XX sequences (SI), given in AAB75803 to AAB76349. (I) has cytostatic,
XX virucide, hepatotropic, antiinflammatory, anti-HIV (human
XX immunodeficiency virus) and protozoacide activities, which can be used
XX in vaccine production and is an inducer of cytotoxic T-cell response.
XX (I) is useful for inducing a cytotoxic T cell response against a
XX preselected antigen in a patient expressing a specific major
XX histocompatibility complex (MHC) class I allele, by contacting cytotoxic
XX T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
XX treat and/or prevent viral infection and cancer such as prostate cancer,
XX hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
XX cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
XX carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
XX acuminatum.
XX
XX Sequence 9 AA;
Query Match 70.0%; Score 35; DB 22; Length 9;
Best Local Similarity 85.7%; Pred. No. 7.8e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 IGHLYL 10
DB 3 IGHLYL 9
RESULT 13
AAW45704
ID AAW45704 standard; peptide; 9 AA.
XX
XX AAW45704;
XX
XX 09-JUN-1998 (first entry)
XX
XX MAGE-2 170 peptide with binding affinity for HLA-B7-like molecules.
XX
XX HLA molecule; cytotoxic T cell; immunogenic peptide; binding affinity;
XX HLA-B7 supermotif; tumour; infection; parasite; CTL; antigen; melanoma;
XX MAGE-2.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9733602-A1.
XX
XX 18-SEP-1997.
XX
XX 10-MAR-1997; 97WO-US03778.
XX
XX 11-MAR-1996; 96US-0013113.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Chestnut RW, Sette A, Sidney J;
XX
XX WPI; 1997-470637/43.

XX Inducing cytotoxic T cell response against specific antigen - using
XX immunogenic peptide with binding affinity for HLA-A3-like molecules,
XX to treat or prevent tumours and infections by virus, parasites etc
XX Example 2; Page 51; 79pp; English.
XX
XX This sequence represents an immunogenic peptide with binding affinity
XX for HLA-B7-like molecules. A cytotoxic T cell (CTL) response against a
XX particular antigen (Ag) is induced in a patient by contacting a CTL with
XX an immunogenic peptide of 9-15 amino acids which binds to at least two
XX HLA-A3-like molecules with dissociation constant less than 500 nM and
XX induces a cytotoxic T cell response. The immunogenic peptide has a
XX sequence of 9 amino acids, comprising a binding motif, with from the
XX N to C-termini: primary anchor sites (PAR) at positions 2 (selected from
XX Ala, Leu, Ile, Val, Met, Ser or Thr) and 9 (Arg or Lys) and at least one
XX secondary anchor sites (SAR), i.e. Tyr, Phe or Trp at positions 3, 6 or
XX 7, and/or Pro at position 8. The immunogenic peptides are used in peptide
XX based vaccines and therapeutic compositions, for treating viral
XX parasitic or fungal diseases or cancer, e.g. prostatic cancer, hepatitis
XX B or C, renal or cervical carcinoma, lymphoma, cytomegalovirus infection
XX or condyloma acuminatum. They can also be used to elicit a CTL response
XX in vitro for subsequent return of the cells to the patient, e.g. where
XX the patient does not respond to peptide vaccines or other therapies.
XX Selection of specific residues for PAR and SAR results in higher binding
XX affinity and thus increased immunogenicity.
XX
XX Sequence 9 AA;
Query Match 66.0%; Score 33; DB 18; Length 9;
Best Local Similarity 77.8%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 VRIGHLYL 10
DB 1 VPISHLYL 9
RESULT 14
AAW46232
ID AAY46232 standard; Peptide; 9 AA.
XX
XX AAY46232;
XX
XX 01-DEC-1999 (first entry)
XX
XX Immunogenic peptide having a human leukocyte antigen binding motif #843.
XX
XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX immune response; T cell activation; major histocompatibility complex;
XX cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX vaccine; immunisation.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX WO9945954-A1.
XX
XX 16-SEP-1999.
XX
XX 13-MAR-1998; 98WO-US05039.
XX
XX 13-MAR-1998; 98WO-US05039.
XX
XX (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX and diagnosis of cancers and viral diseases -

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XX PS Claim 1; Page 62; 150pp; English.
XX CC
XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also
XX CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX CC response against the antigen from which the peptide is derived.
XX CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX CC normally induced by an antigen in the form of a peptide fragment bound
XX CC to a HLA molecule, rather than the intact foreign antigen itself, and
XX CC are particularly important in tumour rejection and in fighting viral
XX CC infections. The peptides are therefore useful therapeutically to treat
XX CC or prevent viral infections and cancers in mammals (especially humans)
XX CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX CC They can be administered as vaccines to elicit an immune response in
XX CC individuals susceptible or otherwise at risk of viral infection or
XX CC cancer, or used to treat chronic or acute conditions. They are also
XX CC useful diagnostically, and can be used to induce a cytotoxic T cell
XX CC response, by contacting a cytotoxic T cell with the peptide e.g. to
XX CC produce CTLs ex vivo for infusion back into a patient. The
XX CC polynucleotides encoding the immunogenic peptides are also useful
XX CC therapeutically and for immunisation as above.
XX CC
XX SQ Sequence 9 AA;
XX SQ
XX SQ Query Match 66.0%; Score 33; DB 20; Length 9;
XX SQ Best Local Similarity 77.8%; Pred. No. 7.8e+05;
XX SQ Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX SQ
XX QY 2 VRIGHLYIL 10
XX Db | | | | |
XX 1 VPISHLYIL 9
XX
XX RESULT 15
XX AAY46263
XX ID AAY46263 standard; Peptide; 9 AA.
XX AC AAY46263;
XX DT 01-DEC-1999 (first entry)
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #874.
XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX KW immune response; T cell activation; major histocompatibility complex;
XX KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX KW vaccine; immunisation.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO945954-A1.
XX PD 16-SEP-1999.
XX PF 13-MAR-1998; 98WO-US05039.
XX PR 13-MAR-1998; 98WO-US05039.
XX PA (EPIM-) EPIMUNE INC.
XX PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
XX PT and diagnosis of cancers and viral diseases -
XX Claim'1; Page 64; 150pp; English.
XX PS

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XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also
XX CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
XX CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
XX CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
XX CC response against the antigen from which the peptide is derived.
XX CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
XX CC normally induced by an antigen in the form of a peptide fragment bound
XX CC to a HLA molecule, rather than the intact foreign antigen itself, and
XX CC are particularly important in tumour rejection and in fighting viral
XX CC infections. The peptides are therefore useful therapeutically to treat
XX CC or prevent viral infections and cancers in mammals (especially humans)
XX CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
XX CC They can be administered as vaccines to elicit an immune response in
XX CC individuals susceptible or otherwise at risk of viral infection or
XX CC cancer, or used to treat chronic or acute conditions. They are also
XX CC useful diagnostically, and can be used to induce a cytotoxic T cell
XX CC response, by contacting a cytotoxic T cell with the peptide e.g. to
XX CC produce CTLs ex vivo for infusion back into a patient. The
XX CC polynucleotides encoding the immunogenic peptides are also useful
XX CC therapeutically and for immunisation as above.
XX CC
XX SQ Sequence 9 AA;
XX SQ
XX SQ Query Match 66.0%; Score 33; DB 20; Length 9;
XX SQ Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX SQ Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX SQ
XX QY 4 IGHLYI 9
XX Db | | | | |
XX 3 IGHLYI 8
XX
XX Search completed: December 19, 2002, 16:50:05
XX Job time : 34 secs

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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:51:44 ; Search time 10 seconds
(without alignments)
16.764 Million cell updates/sec

Title: US-09-692-401-5
Perfect score: 50
Sequence: 1 VVRIGHLIYL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 21193

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	66.0	9	9	US-09-766-889A-58
2	33	66.0	9	9	US-09-017-743C-30
3	33	66.0	9	9	US-09-017-743C-67
4	33	66.0	10	9	US-09-017-743C-115
5	31	62.0	9	9	US-09-017-743C-31
6	29	58.0	8	9	US-09-017-743C-100
7	29	58.0	9	9	US-09-766-889A-18
8	29	58.0	9	9	US-09-766-889A-56
9	29	58.0	9	10	US-09-909-460-51
10	29	58.0	9	10	US-09-812-528-3
11	29	58.0	9	10	US-09-847-185-23
12	29	58.0	9	10	US-09-923-831-6
13	29	58.0	10	9	US-09-766-889A-20
14	29	58.0	10	9	US-09-766-889A-59
15	29	58.0	10	10	US-09-923-831-8
16	28	56.0	9	9	US-09-017-743C-32
17	26	52.0	9	9	US-09-766-889A-7
18	26	52.0	9	12	US-10-026-001-3
19	26	52.0	10	9	US-09-766-889A-6

20	48.0	9	10	US-09-894-018-319	Sequence 319, Appl
21	46.0	7	10	US-09-765-086-79	Sequence 79, Appl
22	46.0	9	9	US-09-826-290-24	Sequence 24, Appl
23	46.0	9	9	US-09-826-290-95	Sequence 95, Appl
24	46.0	9	9	US-09-017-743C-38	Sequence 38, Appl
25	46.0	9	10	US-09-839-497A-13	Sequence 13, Appl
26	46.0	9	10	US-09-791-378-58	Sequence 58, Appl
27	46.0	9	10	US-09-779-308-212	Sequence 212, Appl
28	46.0	9	10	US-09-779-308-608	Sequence 608, Appl
29	46.0	9	10	US-09-779-308-708	Sequence 708, Appl
30	46.0	10	10	US-09-779-308-138	Sequence 138, Appl
31	46.0	10	10	US-09-779-308-346	Sequence 346, Appl
32	46.0	10	10	US-09-779-308-439	Sequence 439, Appl
33	46.0	10	10	US-09-779-308-521	Sequence 521, Appl
34	46.0	10	10	US-09-779-308-525	Sequence 525, Appl
35	46.0	10	10	US-09-779-308-620	Sequence 620, Appl
36	42.0	7	10	US-09-730-801-1	Sequence 1, Appl
37	42.0	8	9	US-09-766-347-1	Sequence 16, Appl
38	42.0	8	10	US-09-756-875-16	Sequence 17, Appl
39	42.0	8	10	US-09-756-875-17	Sequence 6, Appl
40	42.0	9	10	US-09-756-983-6	Sequence 13, Appl
41	42.0	9	10	US-09-756-983-13	Sequence 87, Appl
42	42.0	10	9	US-09-996-288-87	Sequence 98, Appl
43	42.0	10	9	US-09-996-288-98	Sequence 110, Appl
44	42.0	10	9	US-09-996-288-110	Sequence 117, Appl
45	42.0	10	9	US-09-996-288-117	

ALIGNMENTS

RESULT 1
US-09-766-889A-58
; Sequence 58, Application US/09766889A
; Patent No. US2002016454A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-58

Query Match 66.0%; Score 33; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLYI 9
Db 3 IGHLYI 8

RESULT 2
US-09-017-743C-30
; Sequence 30, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro

;
; Sidney, John
; Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-0080500S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-0080500S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-017-743C-30

Query Match 66.0%; Score 33; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 8.9e+04;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VRIGHLYIL 10
| | | | |
Db 1 VPISHLYIL 9

RESULT 3
US-09-017-743C-67
; Sequence 67, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; Sidney, John
; Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-0080500S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>

; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-0080500S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-017-743C-67

Query Match 66.0%; Score 33; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 8.9e+04;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VRIGHLYIL 10
| | | | |
Db 1 VPISHLYIL 9

RESULT 4
US-09-017-743C-115
; Sequence 115, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; Sidney, John
; Southwood, Scott
; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses
; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-0080500S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 115:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-017-743C-115

Query Match 66.0%; Score 33; DB 9; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 2; Indels 0;

QY 2 VRIGHLYL 10
| | | | | | | | | |
Db 1 VPISHLYL 9

RESULT 5
US-09-017-743C-31
; Sequence 31, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; Sidney, John
; Southwood, Scott

; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses

; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-017-743C-31

Query Match 62.0%; Score 31; DB 9; Length 9;
Best Local Similarity 85.7%; Pred. No. 8.9e+04;
Matches 6; Conservative 0; Mismatches 1; Indels 0;

QY 4 IGHLYL 10
| | | | | | | | | |

QY 3 ISHLYL 9

RESULT 6

US-09-017-743C-100
; Sequence 100, Application US/09017743C
; Patent No. US20020177694A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; Sidney, John
; Southwood, Scott

; TITLE OF INVENTION: HLA Binding Peptides and Their
; Uses

; NUMBER OF SEQUENCES: 146
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/017,743C
; FILING DATE: 03-Feb-1998
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/590,298
; FILING DATE: 23-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 018623-008050US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-017-743C-100

Query Match 58.0%; Score 29; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 6; Conservative 0; Mismatches 2; Indels 0;

QY 2 VRIGHLYI 9
| | | | | | | | | |
Db 1 VPISHLYI 8

RESULT 7

US-09-766-889A-18
; Sequence 18, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultze, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104

; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-18

Query Match 58.0%; Score 29; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
Db 5 IGHLY 9

RESULT 8
US-09-766-889A-56
; Sequence 56, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L046177104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-56

Query Match 58.0%; Score 29; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
Db 5 IGHLY 9

RESULT 9
US-09-909-460-51
; Sequence 51, Application US/09909460
; Publication NO. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US/09/321,346

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-460-51

Query Match 58.0%; Score 29; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
Db 5 IGHLY 9

RESULT 10
US-09-812-528-3
; Sequence 3, Application US/09812528
; Patent No. US20010018210A1
; GENERAL INFORMATION:
; APPLICANT: Bachovchin, William
; APPLICANT: Wallner, Barbara
; TITLE OF INVENTION: STIMULATION OF HEMATOPOIETIC CELLS IN
; TITLE OF INVENTION: VITRO
; FILE REFERENCE: I0248/7015
; CURRENT APPLICATION NUMBER: US/09/812,528
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/060,306
; PRIOR FILING DATE: 1997-09-29
; PRIOR APPLICATION NUMBER: US 09/162,934
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-812-528-3

Query Match 58.0%; Score 29; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
Db 5 IGHLY 9

RESULT 11
US-09-847-185-23
; Sequence 23, Application US/09847185
; Patent No. US20020076392A1
; GENERAL INFORMATION:
; APPLICANT: Soo Hoo, William
; TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
; COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
; RESPONSE USING SAME

; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/847,185
; FILING DATE: 01-May-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/201,931
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 2442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-847-185-23

Query Match 58.0%; Score 29; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
Db 5 IGHLY 9

RESULT 12
US-09-923-831-6
; Sequence 6, Application US/09923831
; Patent No. US20020115142A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Val,rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/923,831
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-6

Query Match 58.0%; Score 29; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
Db 5 IGHLY 9

RESULT 13
US-09-766-889A-20
; Sequence 20, Application US/09766889A
; Patent No. US2002016454A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin

;
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-20

Query Match 58.0%; Score 29; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
Db 6 IGHLY 10

RESULT 14
US-09-766-889A-59
; Sequence 59, Application US/09766889A
; Patent No. US2002016454A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-59

Query Match 58.0%; Score 29; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
Db 6 IGHLY 10

RESULT 15
US-09-923-831-8
; Sequence 8, Application US/09923831
; Patent No. US20020115142A1
; GENERAL INFORMATION:
; APPLICANT: Martelange, Val,rie
; APPLICANT: De Smet, Charles
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: L0461/7054
; CURRENT APPLICATION NUMBER: US/09/923,831
; CURRENT FILING DATE: 2001-08-07

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; PRIOR APPLICATION NUMBER: 09/183,706
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-831-8

Query Match      58.0%; Score 29; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 IGHLY 8
        |||||
Db       6 IGHLY 10

Search completed: December 19, 2002, 16:55:47
Job time : 13 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:49:43 : Search time 14 Seconds
(without alignments)
21.016 Million cell updates/sec

Title: US-09-692-401-5
Perfect score: 50
Sequence: 1 VVRIGHLYIL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	84.0	9	1	US-07-938-334C-3
2	42	84.0	9	1	US-08-073-103A-16
3	42	84.0	9	1	US-08-443-341-16
4	42	84.0	9	2	US-08-498-461-15
5	42	84.0	9	3	US-08-498-461-15
6	42	84.0	9	4	US-08-393-273E-16
7	42	84.0	9	4	US-08-443-580F-16
8	42	84.0	10	1	US-08-796-883-30
9	42	84.0	10	3	US-08-602-506A-30
10	31	62.0	9	1	US-08-217-188A-27
11	31	62.0	9	1	US-08-687-226-27
12	31	62.0	9	3	US-08-667-725B-27
13	31	62.0	9	4	US-09-007-748-27
14	29	58.0	9	1	US-07-938-334C-2
15	29	58.0	9	1	US-07-938-334C-4
16	29	58.0	9	1	US-08-073-103A-15
17	29	58.0	9	1	US-08-073-103A-17
18	29	58.0	9	1	US-08-186-266-2
19	29	58.0	9	1	US-08-186-266-4
20	29	58.0	9	1	US-08-186-266-11
21	29	58.0	9	1	US-08-443-341-15
22	29	58.0	9	1	US-08-443-341-17
23	29	58.0	9	1	US-08-787-547-51
24	29	58.0	9	2	US-08-498-461-10
25	29	58.0	9	2	US-08-498-461-11
26	29	58.0	9	2	US-08-902-516-23
27	29	58.0	9	2	US-09-036-582-3

28 29 58.0 9 3 US-08-880-963-18 Sequence 18, Appl
29 29 58.0 9 3 US-08-354-679C-15 Sequence 15, Appl
30 29 58.0 9 3 US-08-354-679C-17 Sequence 17, Appl
31 29 58.0 9 3 US-08-159-339A-576 Sequence 576, Appl
32 29 58.0 9 4 US-09-183-931-27 Sequence 27, Appl
33 29 58.0 9 4 US-09-183-931-33 Sequence 33, Appl
34 29 58.0 9 4 US-08-393-273E-15 Sequence 15, Appl
35 29 58.0 9 4 US-08-393-273E-17 Sequence 17, Appl
36 29 58.0 9 4 US-09-183-706-6 Sequence 6, Appl
37 29 58.0 9 4 US-09-162-934-3 Sequence 3, Appl
38 29 58.0 9 4 US-09-061-388-18 Sequence 18, Appl
39 29 58.0 9 4 US-09-166-448-47 Sequence 47, Appl
40 29 58.0 9 4 US-09-567-995-6 Sequence 6, Appl
41 29 58.0 9 4 US-09-099-543C-18 Sequence 18, Appl
42 29 58.0 9 4 US-09-412-928-18 Sequence 18, Appl
43 29 58.0 9 4 US-08-443-580F-15 Sequence 15, Appl
44 29 58.0 9 4 US-08-443-580F-17 Sequence 17, Appl
45 29 58.0 9 4 US-09-461-083-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-07-938-334C-3
; Sequence 3, Application US/07938334C
; Patent No. 5405940
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
; APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; CITY: 805 Third Avenue
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/938,334C
; FILING DATE: 31-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No 5405940man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: MAGE-21 derived nonapeptide
; US-07-938-334C-3

Query Match 84.0%; Score 42; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVRIGHLY 8
DB 2 VVRIGHLY 9

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RESULT 2
US-08-073-103A-16
; Sequence 16, Application US/08073103A
; Patent No. 5462871
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: De Plaen, Etienne
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Gaugler, Beatrice
; APPLICANT: Van den Eynde, Benoit
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE-3 GENE AND PRESENTED BY HLA-A1 AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073.103A
; FILING DATE: 7-JUNE-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5462871man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-073-103A-16

Query Match 84.0%; Score 42; DB 1; Length 9;
Best Local similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 VVRHGLY 8
Db 2 VVRHGLY 9

RESULT 3
US-08-443-341-16
; Sequence 16, Application US/08443341
; Patent No. 5695994
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: De Plaen, Etienne
; APPLICANT: Lurquin, Christophe
; APPLICANT: Traversari, Catia
; APPLICANT: Gaugler, Beatrice
; APPLICANT: Van den Eynde, Benoit

```

;; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/498,461
; FILING DATE: 5-JULY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5827073man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-498-461-15

Query Match 84.0%; Score 42; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVRIGHLY 8
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Db 2 VVRIGHLY 9

RESULT 5
US-08-354-679C-16
; Sequence 16, Application US/08354679C
; Patent No. 6034214
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
; APPLICANT: De Plaen, Etienne; Lurquin, Christophe; Traversari, Catia
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/354,679C
; FILING DATE: 13-DECEMBER-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAER, MADELINE F.
; REGISTRATION NUMBER: 36,437
; REFERENCE/DOCKET NUMBER: LUD 5293.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-354-679C-16

Query Match 84.0%; Score 42; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVRIGHLY 8
| | | | | | | |
Db 2 VVRIGHLY 9

RESULT 6
US-08-393-273E-16
; Sequence 16, Application US/08393273E
; Patent No. 6222012
; GENERAL INFORMATION:
; APPLICANT: BOON-FALLEUR, Thierry; VAN DER BRUGEN,
; APPLICANT: PLAEN, Etienne; LURQUIN, Christophe; TRAVERSARI, Catia;
; APPLICANT: GAUGLER, Beatrice; VAN DEN EYNDE, Benoit;
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,273E
; FILING DATE: 23-February-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,103
; FILING DATE: 7-June-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-August-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/037,230
; FILING DATE: 26-March-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6222012man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-393-273E-16

Query Match 84.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVRIGHLY 8
| | | | | | | |
Db 2 VVRIGHLY 9

RESULT 7
US-08-443-580F-16
; Sequence 16, Application US/08443580F
; Patent No. 6379901

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;
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; Gaugler, Beatrice; Van den Eynde, Benoît
; TITLE OF INVENTION: Method For Screening For Cancer
; Using Binders For MAGE Related Peptides And Complexes
; Of The Peptide And HLA Molecules
;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM, PH.D./2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,580F
; FILING DATE: 17-May-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,103
; FILING DATE: 7-JUNE-1993
; APPLICATION NUMBER: 07/938,334
; FILING DATE: 31-AUGUST-1992
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6379901man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5293.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-443-580F-16

Query Match 84.0%; Score 42; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVRIGHLY 8
Db 2 VVRIGHLY 9

RESULT 8
US-08-796-883-30
; Sequence 30, Application US/08796883
; Patent No. 5744353
; GENERAL INFORMATION:
; APPLICANT: Herman, Jean; Coulie, Pierre;
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Luescher, Immanuel.
; TITLE OF INVENTION: Tumor Rejection Antigens Presented By
; TITLE OF INVENTION: HLA-B44 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
```

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;
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,883
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,506
; FILING DATE: 20-FEBRUARY-1996
; APPLICATION NUMBER: 08/531,864
; FILING DATE: 21-SEPTEMBER-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,636
; FILING DATE: 17-JANUARY-1995
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,503
; FILING DATE: 3-JUNE-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5744353man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Mage-12/HLA-B44
US-08-796-883-30

Query Match 84.0%; Score 42; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVRIGHLY 8
Db 3 VVRIGHLY 10

RESULT 9
US-08-602-506A-30
; Sequence 30, Application US/08602506A
; Patent No. 6060257
; GENERAL INFORMATION:
; APPLICANT: Herman, Jean; Coulie, Pierre;
; APPLICANT: Boon-Falleur, Thierry; van der Bruggen, Pierre;
; APPLICANT: Luescher, Immanuel.
; TITLE OF INVENTION: Tumor Rejection Antigens Presented By HLA-
; TITLE OF INVENTION: B44 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,506A
; FILING DATE: 20-FEBRUARY-1996
; CLASSIFICATION: 435
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;; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/531,864
; FILING DATE: 21-SEPTEMBER-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,636
; FILING DATE: 17-JANUARY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/253,503
; FILING DATE: 3-JUNE-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6060257man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5436
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Mage-12/HLA-B44
; US-08-602-506A-30

Query Match 84.0%; Score 42; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVRIGLY 8
| | | | | | | |
Db 3 VVRIGLY 10

RESULT 10
US-08-217-188A-27
; Sequence 27, Application US/08217188A
; Patent No. 5554724
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor Mage-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,188A
; FILING DATE: 24-MARCH-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5554724man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-217-188A-27

Query Match 62.0%; Score 31; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 IGHLYIL 10
| | | | |
Db 2 ISHLYIL 8

RESULT 11
US-08-687-226-27
; Sequence 27, Application US/08687226
; Patent No. 5686068
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.; Visseren, M. W.;
; APPLICANT: van der Burg, Sjoerd; van der Bruggen, Pierre;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Derived From
; TITLE OF INVENTION: Mage-2, Cytolytic T Cells Specific To Complexes Of
; TITLE OF INVENTION: Peptides And HLA-A2 Molecules, And Uses Thereof
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,226
; FILING DATE: 25-JULY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/217,188
; FILING DATE: 24-MARCH-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5686068man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5447
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-687-226-27

Query Match 62.0%; Score 31; DB 1; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 IGHLYIL 10
| | | | |
Db 2 ISHLYIL 8

RESULT 12
US-08-667-725B-27
; Sequence 27, Application US/08667725B

```
; Patent No. 6063900
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/667,725B
; FILING DATE: 21 June 1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6063900man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.1 DIV (081585)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-667-725B-27

Query Match 62.0%; Score 31; DB 3; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGHLYIL 10
Db 2 ISHLYIL 8

RESULT 13
US-09-007-748-27
; Sequence 27, Application US/09007748
; Patent No. 6147187
; GENERAL INFORMATION:
; APPLICANT: Melief, Cornelis J. M.
; APPLICANT: Visseren, M. J. W.
; APPLICANT: Kast, W. M.
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Tumor Rejection Antigen
; TITLE OF INVENTION: Precursor MAGE-2 Derived Peptides, and Uses Thereof
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
```

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; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,748
; FILING DATE: 15 January 1998
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6147187man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5340.2 DIV (081572)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-007-748-27

Query Match 62.0%; Score 31; DB 4; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGHLYIL 10
Db 2 ISHLYIL 8

RESULT 14
US-07-938-334C-2
; Sequence 2, Application US/07938334C
; Patent No. 5405940
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
; APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/938,334C
; FILING DATE: 31-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5405940man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: MAGE-2 derived nonapeptide
; US-07-938-334C-2
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Query Match 58.0%; Score 29; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVRIGHLY 8
|||
Db 2 VVPISHLY 9

RESULT 15

US-07-938-334C-4
; Sequence 4, Application US/07938334C
; Patent No. 5405940
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry; van der Bruggen, Pierre;
; APPLICANT: De Plaen, Etienne; Lurquin Christophe; Traversari, Catia
; TITLE OF INVENTION: ISOLATED NONAPEPTIDES DERIVED FROM
; TITLE OF INVENTION: MAGE GENES AND USES THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/938,334C
; FILING DATE: 31-AUG-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5405940man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: MAGE-3 derived nonapeptide
US-07-938-334C-4

Query Match 58.0%; Score 29; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHLY 8
|||||
Db 5 IGHLY 9

Search completed: December 19, 2002, 16:52:37
Job time : 33 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:49:09 ; Search time 15 seconds
(without alignments)
64.090 Million cell updates/sec

Title: US-09-692-401-5
Perfect score: 50
Sequence: 1 VWRIGHLIYL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%	Query Match	Length	DB ID	Description
1	21	42.0	10	2	PQ0177	neuromedin C - lau
2	21	42.0	10	2	A60647	neuromedin C - bov
3	20	40.0	10	2	A59173	nuclease Bhl (EC 3
4	19	38.0	10	2	A30823	bothropstoxin - ja
5	17	34.0	4	2	I38888	COI intron 16 prot
6	17	34.0	9	2	S07205	litorin 2-Glu - Au
7	17	34.0	9	2	S07204	litorin I - Austr
8	17	34.0	9	2	S39437	D-amino-acid oxida
9	17	34.0	10	2	S74176	gluconokinase (EC
10	16	32.0	10	1	GMROL2	leucosulfakinin-II
11	16	32.0	10	2	A32543	cardioexcitatory n
12	16	32.0	10	2	B46453	e antigen p20e pre
13	16	32.0	10	2	B60656	leucosulfakinin II
14	16	32.0	10	2	A56633	neomycinopressin -
15	15	30.0	4	2	PL0140	carbon monoxide de
16	15	30.0	7	2	A28709	phosphonoacetaldeh
17	15	30.0	9	2	PT0238	lg heavy chain CRD
18	15	30.0	10	2	T14212	cytochrome-c oxida
19	15	30.0	10	2	S74147	glyceraldehyde-3-p
20	14	28.0	3	3	GKHU	growth-modulating
21	14	28.0	6	2	A61419	sarcosine dehydrog
22	14	28.0	6	2	B56979	collagen alpha 1(I
23	14	28.0	7	1	NYPG7	hypothalamic hepta
24	14	28.0	7	2	S42407	gramicidin S synth
25	14	28.0	8	2	A61467	penalbumin - Adeli
26	14	28.0	9	2	S07241	litorin - Rohde's
27	14	28.0	10	2	A61289	streptopain (EC 3.
28	14	28.0	10	2	XGHUE	erythrocyte membra
29	13	26.0	4	2	PT0721	T-cell receptor be

30	13	26.0	7	2	A60139	fatty-acid synthas
31	13	26.0	7	2	PQ0663	membrane protein -
32	13	26.0	7	2	A25269	sex pheromone CAM3
33	13	26.0	7	4	I56695	hypothetical U2 pr
34	13	26.0	9	2	S78420	ribosomal protein
35	13	26.0	10	2	S13224	virg protein - Agr
36	13	26.0	10	2	S06964	hypothetical prote
37	13	26.0	10	2	S68033	cytochrome P450 1A
38	13	26.0	10	2	T12312	cytochrome-c oxida
39	13	26.0	10	2	A44871	monodehydroascorba
40	12	24.0	4	2	A48360	gamma subunit of p
41	12	24.0	6	2	A60986	N-formyl oligopept
42	12	24.0	7	2	S45311	microcin C7 - Esch
43	12	24.0	8	2	B45800	serum albumin - do
44	12	24.0	8	2	PC4373	telomeric and tetr
45	12	24.0	9	2	S13636	coat protein beta

ALIGNMENTS

RESULT 1
PQ0177
neuromedin C - laughing frog
C:Species: Rana ridibunda (laughing frog)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 11-Jan-2000
C:Accession: PQ0177
R:Conlon, J.M.; O'Harte, F.; Vaudry, H.
Biochem. Biophys. Res. Commun. 178, 526-530, 1991
A:Title: Primary structures of the bombesin-like neuropeptides in frog brain show the
A:Reference number: PQ0177; MUID:91315477; PMID:18559413
A:Accession: PQ0177
A:Molecule type: protein
A:Residues: 1-10 <CON>
A:Experimental source: brain
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end
F:10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 42.0%; Score 21; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHL 7
DB 6 VGHL 9

RESULT 2
A60647
neuromedin C - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
C:Accession: A60647
R:Lemaire, S.; Trifaro, J.M.; Chouinard, L.; Cecyre, D.; Dessureault, J.; Mercier, P.
Peptides 10, 355-360, 1989
A:Title: Structural identification, subcellular localization and secretion of bovine
A:Reference number: A60647; MUID:89331342; PMID:2755876
A:Accession: A60647
A:Molecule type: protein
A:Residues: 1-10 <LEM>
A:Note: this neuropeptide was purified from secretory granules of cells in the adrena
C:Superfamily: gastrin-releasing peptide
C:Keywords: adrenal gland; neuropeptide

Query Match 42.0%; Score 21; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHL 7
DB 6 VGHL 9

```
RESULT 3
A59173
nuclease Bhl (EC 3.1.-.-) - Basidiobolus haptosporus (fragment)
C:Species: Basidiobolus haptosporus
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: A59173
R:Desai, N.; Shankar, V.
submitted to the Protein Sequence Database, February 2000
A:Description: Single-strand-specific, guanylic acid preferential nuclease from Basidiobolus haptosporus
A:Reference number: A59173
A:Accession: A59173
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <DES>
A:Note: extracellular, single-strand-specific nuclease
C:Keywords: hydrolase

Query Match 40.0%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.5e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGH 7
Db 4 LGHL 7

RESULT 4
A30823
bothropstoxin - jararacussu (fragment)
C:Species: Bothrops jararacussu (jararacussu)
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C:Accession: A30823
R:Honsi-Brandeburgo, M.I.; Queiroz, L.S.; Santo-Neto, H.; Rodrigues-Simioni, L.; Giglio,
Toxicon 26, 615-627, 1988
A:Title: Fractionation of Bothrops jararacussu snake venom: partial chemical characterization
A:Reference number: A30823; MUID:89020120; PMID:3176051
A:Accession: A30823
A:Molecule type: protein
A:Residues: 1-10 <HOW>

Query Match 38.0%; Score 19; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 1e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGHLYI 9
Db 5 LGHML 10

RESULT 5
I38888
CoI intron 16 protein - Podospora anserina mitochondrion
C:Species: mitochondrion Podospora anserina
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999
C:Accession: I38888
R:Cummings, D.J.; Michel, F.; McNally, K.L.
Curr. Genet. 16, 381-406, 1989
A:Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit I mRNA
A:Reference number: A48327; MUID:90124722; PMID:2558809
A:Accession: I38888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <CUM>
A:Cross-references: GB:X55026; GB:M30937; GB:M61734
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC3
C:Keywords: mitochondrion

Query Match 34.0%; Score 17; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
S07205
litorin 2-Glu - Australian tree frog (Litoria aurea)
C:Species: Litoria aurea
C:Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07205
R:Anastasi, A.; Montecucchi, P.; Angelucci, F.; Erspamer, V.; Endeian, R.
Experientia 33, 1289, 1977
A:Title: Glu(OMe)(2)-litorin, the second bombesin-like peptide occurring in methanol
A:Reference number: S07205; MUID:78003546; PMID:908397
A:Accession: S07205
A:Molecule type: protein
A:Residues: 1-9 <ANA>
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGH 6
Db 5 VGH 7

RESULT 7
S07204
litorin 1 - Australian tree frog (Litoria aurea)
C:Species: Litoria aurea
C:Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C:Accession: S07204
R:Anastasi, A.; Erspamer, V.; Endeian, R.
Experientia 31, 510-511, 1975
A:Title: Aminoacid composition and sequence of litorin, a bombesin-like nonapeptide f
A:Reference number: S07204; MUID:75187011; PMID:1140241
A:Accession: S07204
A:Molecule type: protein
A:Residues: 1-9 <ANA>
C:Superfamily: gastrin-releasing peptide
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGH 6
Db 5 VGH 7

RESULT 8
S39437
D-amino-acid oxidase (EC 1.4.3.3) - Trigonopsis variabilis (fragment)
C:Species: Trigonopsis variabilis
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1997 #text_change 07-May-1999
C:Accession: S39437
R:Schraeder, T.; Andreesen, J.R.
Eur. J. Biochem. 218, 735-744, 1993
A:Title: Evidence for the functional importance of Cys298 in D-amino acid oxidase fro
A:Reference number: S39437; MUID:94094889; PMID:7903639
A:Accession: S39437
A:Molecule type: protein
A:Residues: 1-9 <SCH>
```

A:Experimental source: CBS 4095

C:Function:

C:Species: Schistosoma gregaria (desert locust)
C:Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 18-Aug-2000
C:Keywords: FAD; oxidoreductase

Query Match 34.0%; Score 17; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGH 6

DB 2 VGH 4

RESULT 9

S74176

glucokinase (EC 2.7.1.12), thermoresistant - Escherichia coli (fragment)

C:Species: Escherichia coli

C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999

C:Accession: S74176

R:izu, H.; Adachi, O.; Yamada, M.

FEBS Lett. 394, 14-16, 1996

A:Title: Purification and characterization of the Escherichia coli thermoresistant glucokinase

A:Accession: S74176

A:Molecule type: protein

A:Residues: 1-10 <IZU>

A:Experimental source: strain K-12

C:Genetics:

A:Gene: gntK

C:Keywords: dimer; phosphotransferase

Query Match 34.0%; Score 17; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.6e+03;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HLX 8

DB 8 HIY 10

RESULT 10

GMROL2

leucosulfakinin-II - Madeira cockroach

N:Alternate names: LSK-II

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 13-Sep-1996

C:Accession: A26335

R:Nachman, R.J.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.

Biochem. Biophys. Res. Commun. 140, 357-364, 1986

A:Title: Leucosulfakinin-II, a blocked sulfated insect neuro peptide with homology to cholecystinin

A:Reference number: A26335; PMID:87048769; PMID:3778455

A:Accession: A26335

A:Molecule type: protein

A:Residues: 1-10 <NAC>

C:Comment: This peptide was isolated from head extracts. It stimulates muscle contraction

C:Superfamily: gastrin

C:Keywords: amidated carboxyl end; neuro peptide; pyroglutamic acid; sulfoliprotein

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:5/Binding site: sulfate (Tyr) (covalent) #status experimental

F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.0%; Score 16; DB 1; Length 10;

Best Local Similarity 66.7%; Pred. No. 4.1e+03;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GHL 7

DB 6 GHM 8

RESULT 11

A32543

cardioexcitatory neuro peptide - desert locust

C:Species: Schistosoma gregaria (desert locust)

C:Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 18-Aug-2000

C:Accession: A32543

R:Robb, S.; Packman, L.C.; Evans, P.D.

Biochem. Biophys. Res. Commun. 160, 850-856, 1989

A:Title: Isolation, primary structure and bioactivity of Schistosoma gregaria neuro peptide

A:Reference number: A32543; PMID:89246543; PMID:2719702

A:Accession: A32543

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <POB>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; neuro peptide

F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.0%; Score 16; DB 2; Length 10;

Best Local Similarity 16.7%; Pred. No. 4.1e+03;

Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGHLYI 9

DB 3 VDHVEL 8

RESULT 12

B46453

e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)

N:Alternate names: HBe antigen precursor

C:Species: hepatitis B virus, HBV

A:Variety: subtype adr

C:Date: 18-Jun-1993 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997

C:Accession: B46453

R:Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Ts

J. Immunol. 147, 3156-3160, 1991

A:Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of h

A:Reference number: A46453; PMID:92013147; PMID:171758

A:Accession: B46453

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <TAK>

A:Experimental source: subtype adr

A:Note: sequence extracted from NCBI backbone (NCBI:60243)

F:1-10/Domain: signal sequence (fragment) #status predicted <SIG>

Query Match 32.0%; Score 16; DB 2; Length 10;

Best Local Similarity 22.2%; Pred. No. 4.1e+03;

Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 VRIGHLYIL 10

DB 1 MOLFHLLXI 9

RESULT 13

B60656

leucosulfakinin II, non-sulfated - American cockroach

C:Species: Periplaneta americana (American cockroach)

C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 08-Dec-1995

C:Accession: B60656

R:Veenstra, J.A.

Neuropeptides 14, 145-149, 1989

A:Title: Isolation and structure of two gastrin/CCCK-like neuropeptides from the Ameri

A:Reference number: A60656; PMID:90137190; PMID:2615921

A:Accession: B60656

A:Molecule type: protein

A:Residues: 1-10 <VEE>

C:Keywords: amidated carboxyl end; neuro peptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:10/Modified site: amidated carboxyl end (Phe) #status experimental

```

Query Match      32.0%; Score 16; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GHL 7
Db 6 GHM 8

RESULT 14
A56633
neomysosuppressin - flesh fly (Sarcophaga bullata)
N:Alternate names: Neb-MS
C:Species: Sarcophaga bullata
C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Jun-2000
C:Accession: A56633
R:Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; Bueds, H.; De Loof, A.
Comp. Biochem. Physiol. C 102, 239-245, 1992
A:Title: Isolation, primary structure and synthesis of neomysosuppressin, a myoinhibiting
A:Reference number: A56633; MUID:93047886; PMID:1358537
A:Accession: A56633
A:Molecule type: protein
A:Residues: 1-10 <FON>
A:Experimental source: head
A:Note: sequence extracted from NCBI backbone (NCBIP:119072)
C:Keywords: amidated carboxyl end; neuropeptide
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match      32.0%; Score 16; DB 2; Length 10;
Best Local Similarity 16.7%; Pred. No. 4.1e+03;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGHLYI 9
Db 3 VDHVEL 8

RESULT 15
PL0140
carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena
C:Species: Pseudomonas carboxydohydrogena
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C:Accession: PL0140
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrog
A:Reference number: PL0138; MUID:90055678; PMID:2818128
A:Accession: PL0140
A:Molecule type: protein
A:Residues: 1-4 <KRA>
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
C:Keywords: oxidoreductase

Query Match      30.0%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGH 6
Db 1 MGH 3

Search completed: December 19, 2002, 16:51:58
Job time : 16 secs

```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:46:03 ; Search time 10 Seconds
(without alignments)
41.476 Million cell updates/sec

Title: US-09-692-401-5
Perfect score: 50
Sequence: 1 VVRIGHLVIL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 346

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	21	42.0	10	1	GRP_RANRI	P23260 rana ridibu
2	17	34.0	9	1	LITO_LITAU	P08945 litoria aur
3	16	32.0	9	1	NEUX_HUMAN	P04277 homo sapien
4	16	32.0	9	1	NSK1_SARBU	P41492 sarcophaga
5	16	32.0	10	1	FARP_LOCFI	P38553 locusta mig
6	16	32.0	10	1	LCMS_LEUMA	P21144 leucophaea
7	16	32.0	10	1	LSK2_LEUMA	P09039 leucophaea
8	16	32.0	10	1	NEMS_DROME	P41494 drosophila
9	15	30.0	4	1	DCML_PSECH	P19916 pseudomonas
10	14	28.0	3	1	GRWM_HUMAN	P01157 homo sapien
11	14	28.0	7	1	FAR2_ASCSU	P31890 ascaris suu
12	14	28.0	7	1	HY7_PIG	P01153 sus scrofa
13	14	28.0	9	1	LITR_PHYRO	P08946 phylomedus
14	14	28.0	10	1	GLEM_HUMAN	P02728 homo sapien
15	13	26.0	7	1	CIA_ENTFA	P11932 enterococcu
16	13	26.0	7	1	GFRP_MOUSE	P99025 mus muscucu
17	13	26.0	9	1	PGLR_DIAAB	P81179 diatrepes a
18	12	24.0	8	1	ANG2_BOTJA	Q10582 bothrops ja
19	12	24.0	9	1	MOSH_CLYJA	P19852 clypeaster
20	12	24.0	9	1	RE42_LITRU	P82075 litoria rub
21	12	24.0	9	1	RS10_SERMA	O68936 serratia ma
22	12	24.0	10	1	ANGT_BOVIN	P01017 bos taurus
23	11	22.0	5	1	FARP_ARTTR	P41853 artiposthi
24	11	22.0	5	1	PSK_DAUCA	P58261 daucus caro
25	11	22.0	7	1	UN06_PINPS	P81675 pinus pinas
26	11	22.0	8	1	ALL6_CXDPO	P82157 cydia pomon
27	11	22.0	9	1	CONO_CONST	P05487 conus stria
28	11	22.0	9	1	ISOT_CYPCA	P42993 cyprinus ca
29	11	22.0	9	1	NEUU_CAVPO	P34966 cavia porce
30	11	22.0	9	1	OXYA_SCYCA	P42996 scyllorhinu
31	11	22.0	9	1	OXYA_SQUAC	P42999 squalus aca
32	11	22.0	9	1	OXYT_BUFRE	P42995 bufo regula
33	11	22.0	9	1	OXYT_CYPCA	P23879 cyprinus ca

34	11	22.0	9	1	OXYT_RABIT	P32878 oryctolagus
35	11	22.0	9	1	OXYT_RAJCL	P42994 raja clavat
36	11	22.0	9	1	OXYV_SQUAC	P43000 squalus aca
37	11	22.0	10	1	ANG1_BOTJA	Q10581 bothrops ja
38	11	22.0	10	1	ANGT_CHICK	P01018 gallus gall
39	11	22.0	10	1	FARP_MANSE	P18523 manduca sex
40	11	22.0	10	1	FARP_MITED	P42360 mytilus edu
41	11	22.0	10	1	UPAS_HUMAN	P30091 homo sapien
42	11	22.0	10	1	UXA6_CHLTR	P38007 chlamydia t
43	10	20.0	5	1	TPIS_CANFA	P54714 canis famil
44	10	20.0	5	1	UF01_MOUSE	P38639 mus musculu
45	10	20.0	6	1	FARP_MONEX	P41966 moniezia ex

ALIGNMENTS

RESULT 1
GRP_RANRI STANDARD; PRT; 10 AA.
AC P23260;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuromedin C.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE
RC TISSUE=Brain;
RX MEDLINE=91315477; PubMed=1859413;
RA Conlon J.M., O'Harte F., Vaudry H.;
RT "Primary structures of the bombesin-like neuropeptides in frog brain
show that bombesin is not the amphibian gastrin-releasing peptide.";
RL Biochem. Biophys. Res. Commun. 178:526-530(1991).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
CC PIR; P00177; P00177.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1094 MW; F81FBAE862CDC371 CRC64;
Query Match 42.0%; Score 21; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGHL 7
: : : :
Db 6 VGHL 9

RESULT 2
LITO_LITAU STANDARD; PRT; 9 AA.
ID LITO_LITAU
AC P08945;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Litoria.
OS Litoria aurea (Green and golden bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=8371;
RN [1]
RP SEQUENCE.
RX MEDLINE=75187011; PubMed=1140241;

```
RA Anastasi A., Ersperer V., Endean R.;
RT "Aminoacid composition and sequence of litorin, a bombesin-like
RT nonapeptide from the skin of the Australian leptodactylid frog
RT Litoria aurea.";
RL Experientia 31:510-511(1975).
RN [2]
RN SEQUENCE (METHYLATED VARIANT).
RX MEDLINE=78003546; PubMed=908397;
RA Anastasi A., Montecucchi P.C., Angelucci F., Ersperer V., Endean R.;
RT "Glu(OMe)3-litorin, the second bombesin-like peptide occurring in
RT methanol extracts of the skin of the Australian frog Litoria aurea.";
RL Experientia 33:1289-1289(1977).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR; S07204; S07204.
DR PIR; S07205; S07205.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin; 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation; Methylation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 2 2 METHYLATION (IN A VARIANT).
FT MOD_RES 9 9 AMIDATION.
FT SEQUENCE 9 AA; 1103 MW; D/CCCLIE862CDC366 CRC64;
SQ
Query Match 34.0%; Score 17; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 IGH 6
DB 5 VGH 7
[1]
[2]
RESULT 3
NEUX_HUMAN
ID NEUX_HUMAN STANDARD; PRT; 9 AA.
AC P04277;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotensin-related peptide (NRP) (Kinetensin).
OS Homo sapiens (Human).
OS Bos taurus (Bovine), and
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606, 9913, 9986;
RN [1]
RN SEQUENCE.
RC SPECIES=Human;
RX MEDLINE=86242180; PubMed=3087352;
RA Mogard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,
RA Shively J.E., Walsh J.H.;
RT "The amino acid sequence of kinetensin, a novel peptide isolated from
RT pepsin-treated human plasma: homology with human serum albumin,
RT neurotensin and angiotensin.";
RL Biochem. Biophys. Res. Commun. 136:983-988(1986).
RN [2]
RN SEQUENCE.
RC SPECIES=Human, Bovine, and Rabbit;
RX MEDLINE=87194805; PubMed=2437111;
RA Carraway R.E., Mitra S.P., Cochrane D.E.;
RT "Structure of a biologically active neurotensin-related peptide
RT obtained from pepsin-treated albumin(s).";
RL J. Biol. Chem. 262:5968-5973(1987).
CC -!- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND
CC BLOOD FLOW (POTENTIAL).
DR PIR; A03239; ABHUSK.
DR PIR; A26693; A26693.
KW Hormone.
SQ SEQUENCE 9 AA; 1172 MW; C804DB4761F4140D CRC64;
```

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Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 HLYIL 10
DB 5 HPYFL 9
[1]
[2]
RESULT 4
NSKI_SARBU
ID NSKI_SARBU STANDARD; PRT; 9 AA.
AC P41492;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Neosulfakinin-I (NEB-SK-I).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Oestroidea; Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RN SEQUENCE.
RC TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RT the fleshfly, Neobellieria bullata.";
RL Comp. Biochem. Physiol. 103C:135-142(1992).
CC -!- FUNCTION: MYOTROPIC PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Neuropeptide; Amidation; Sulfation.
FT MOD_RES 4 4 SULFATION (POTENTIAL).
FT MOD_RES 9 9 AMIDATION (POTENTIAL).
FT SEQUENCE 9 AA; 1187 MW; 8B0A0691E86B5AAA CRC64;
SQ
Query Match 32.0%; Score 16; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 GHL 7
DB 5 GHM 7
[1]
[2]
RESULT 5
FARP_LOCFI
ID FARP_LOCFI STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistofuramide (PDVDFLRF-amide) (Cardioexcitatory neuropeptide).
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004, 7010;
RN [1]
RN SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelincx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PDVDFLRFamide
RT (Schistofuramide) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct.";
```

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RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX MEDLINE=80246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistostylr-f-amide, a
  FMRF-amide-like neuropeptide from the locust, Schistocerca
  gregaria.";
RT Biochem. Biophys. Res. Commun. 160:850-856(1989).
RL NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
  OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
  OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
  THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
  FAMILY.
DR PIR; A32543; A32543.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;
Best Local Similarity 16.7%; Pred. No. 1.8e+03;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGHLYI 9
: |:::
Db 3 VDHVFL 8

RESULT 6
LCMS_LEUMA
ID LCMS_LEUMA STANDARD; PRT; 10 AA.
AC P21144; P41497;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Leucomyosuppressin (LMS) (LeM-MS).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucomyosuppressin,
  an insect neuropeptide that inhibits spontaneous contractions of the
  cockroach hindgut.";
RL Comp. Biochem. Physiol. 85C:329-333(1986).
CC -!- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH
  PROTODEUM (HINDGUT).
CC Neuropeptide; Amidation.
FT MOD_RES 1 1
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;
Best Local Similarity 16.7%; Pred. No. 1.8e+03;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGHLYI 9
: |:::
Db 3 VDHVFL 8

RESULT 7
LSK2_LEUMA
ID LSK2_LEUMA STANDARD; PRT; 10 AA.
AC P09039;
DT 01-NOV-1988 (Rel. 09, Created)

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DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Leucosulfakinin-II (LSK-II).
OS Leucophaea maderae (Madeira cockroach), and
  Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6978;
RN [1]
RP SEQUENCE.
RC SPECIES=L.maderae;
RX MEDLINE=87048769; PubMed=3778455;
RA Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
RT "Leucosulfakinin-II, a blocked sulfated insect neuropeptide with
  homology to cholecystokinin and gastrin.";
RL Biochem. Biophys. Res. Commun. 140:357-364(1986).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana; TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CKK-like neuropeptides from
  the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -!- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF
  THE COCKROACH HINDGUT. STIMULATES MUSCLE CONTRACTION OF HINDGUT.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR PIR; A26335; GMROL2.
DR PIR; B60656; B60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 1 1
FT MOD_RES 5 5
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1255 MW; 9B4F5391E86B5AAA CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GHL 7
: |::
Db 6 GHM 8

RESULT 8
NEMS_DROME
ID NEMS_DROME STANDARD; PRT; 10 AA.
AC P41494;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dromyosuppressin (Neomyosuppressin) (NEB-MS).
GN DMS OR NEMS.
OS Drosophila melanogaster (Fruit fly), and
  Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227, 7385;
RN [1]
RP SEQUENCE.
RC SPECIES=D.melanogaster;
RX MEDLINE=93002195; PubMed=1390001;
RA Nichols R.;
RT "Isolation and structural characterization of Drosophila
  TDVDFVFLRFamide and EMRFamide-containing neural peptides.";
RL J. Mol. Neurosci. 3:213-218(1992).
RN [2]
RP SEQUENCE.

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RC SPECIES=S.bullata; TISSUE=Head;
RX MEDLINE=93047886; PubMed=1358537;
RA Fonagy A., Schoofs L., Proost P., Van Damme J., Bueds H., De Loof A.;
RT "Isolation, primary structure and synthesis of neomyosuppressin, a
RT myoinhibiting neuropeptide from the grey fleshfly, Neobellieria
RT bullata.";
RL Comp. Biochem. Physiol. 102C:239-245(1992).
CC -!- FUNCTION: MYOINHIBITING NEUROPEPTIDE.
DR Flybase; FBgn0011581; Dms.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1248 MW; D3C00329D2C1EAB2 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 10;
Best Local Similarity 16.7%; Pred. No. 1.8e+03;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGHLYI 9
DB 3 VDHVEL 8

RESULT 9
DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain [EC 1.2.99.2] (CO
DE dehydrogenase subunit L) (CO-DH L) (fragment).
GN CuriL.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydophilic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; P0140; P0140.
KW Oxidoreductase; Molybdenum.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. NO. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 IGH 6
DB 1 MGH 3

RESULT 10
GRWM_HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR PIR; A01421; GRHU.
SQ SEQUENCE 3 AA; 340 MW; 6331E8100000000000 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GH 6
DB 1 GH 2

RESULT 11
FAR2_ASCSU STANDARD; PRT; 7 AA.
ID FAR2_ASCSU
AC P31890;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF2.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253, 6233;
RN [1]
RP SEQUENCE.
RC SPECIES=A.suum;
RX MEDLINE=93324431; PubMed=8332542;
RA Cowden C., Stretton A.O.W.;
RT "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
RL Peptides 14:423-430(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=P.redivivus;
RX MEDLINE=95060998; PubMed=7970891;
RA Maule A.G., Shaw C., Bowman J.W.;
RT "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the
RT free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";
RL Parasitology 109:351-356(1994).
CC -!- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.
CC -!- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7
SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 HLYI 9
DB 2 HEYL 5

RESULT 12
HY7_PIG STANDARD; PRT; 7 AA.
ID HY7_PIG
AC P01153;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Hypothalamic heptapeptide.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE. AND SYNTHESIS
RX MEDLINE=81213980; PubMed=6263778;
RA Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA Saifran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT "Isolation, structure and synthesis of a heptapeptide with in vitro
RT ACTH-releasing activity from porcine hypothalamus.";
RL Horm. Metab. Res. 13:228-232(1981).
DR PIR: A01417; NYPG7
SQ SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 IGHLY 8
DB 2 IYHSY 6

RESULT 13
LITR_PHYRO
ID LITR_PHYRO STANDARD; PRT; 9 AA.
AC P08946;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rhodei-litorin.
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RP SEQUENCE.
RX MEDLINE=85127560; PubMed=3838283;
RA Barra D., Erspamer G.F., Simmaco M., Bossa F., Melchiorri P.,
RA Erspamer V.;
RT "Rhodei-litorin: a new peptide from the skin of Phyllomedusa rohdei.";
RL FEBS Lett. 182:53-56(1985).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN
CC FAMILY.
DR PIR: S07241; S07241.
DR InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin; 1.
DR PROSITE: PS00257; BOMBESIN; 1.
KW Bombesin family; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1090 MW; 4ECCCL1E861ADC377 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GH 6
DB 6 GH 7

RESULT 14
GLEM_HUMAN
ID GLEM_HUMAN STANDARD; PRT; 10 AA.
AC P02728;
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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Erythrocyte membrane glycopeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72034940; PubMed=5286858;
RA Weiss J.B., Lote C.J., Bobinski H.;
RT "New low molecular weight glycopeptide containing triglycosylcysteine
RT in human erythrocyte membrane.";
RL Nature New Biol. 234:25-26(1971).
CC -|- PFM: S-LINKED GLYCAN CONSISTS OF GLC-GLC-GLC TRISACCHARIDE.
CC -|- MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS
CC PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED.
DR PIR: A03187; XGHUE
KW Glycoprotein; Erythrocyte.
FT CARBOHYD 1 1 S-LINKED (GLC... ).
SQ SEQUENCE 10 AA; 1049 MW; 239BFEAA1F5B1E8 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GH 6
DB 3 GH 4

RESULT 15
CIA_ENTFA
ID CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAM373 (clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT CAM373.";
RL FEBS Lett. 206:69-72(1986).
CC -|- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
CC HARBORING PAM373.
CC -|- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
CC -|- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR: A25269; A25269.
KW Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 26.0%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 LYIL 10
DB 2 IFIL 5

Search completed: December 19, 2002, 16:50:37
Job time : 24 secs
```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:48:49 ; Search time 37 Seconds
(without alignments)
55.688 Million cell updates/sec

Title: US-09-692-401-5

Perfect score: 50

Sequence: 1 VVRIGHLYIL 10

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	48.0	7	10 P82445	P82445 nicotiana t
2	19	38.0	9	4 Q14277	Q14277 homo sapien
3	17	34.0	7	12 Q9YQ10	Q9YQ10 transmissib
4	16	32.0	8	2 Q93SP2	Q93SP2 pseudomonas
5	16	32.0	10	2 P83066	P83066 bacillus ce
6	16	32.0	10	4 Q96Q19	Q96Q19 homo sapien
7	16	32.0	10	12 Q9PXC3	Q9PXC3 hepatitis b
8	15	30.0	8	8 Q9XNP8	Q9XNP8 boophilus m
9	15	30.0	10	2 P83161	P83161 anabaena sp
10	15	30.0	10	6 Q95NB1	Q95NB1 eulemur ful
11	15	30.0	10	6 Q95NB0	Q95NB0 eulemur ful
12	15	30.0	10	8 P92762	P92762 uromastix a
13	14	28.0	8	3 Q05403	Q05403 saccharomyc
14	14	28.0	9	2 Q47410	Q47410 escherichia
15	14	28.0	9	4 Q9H4M8	Q9H4M8 homo sapien
16	14	28.0	9	5 Q9VW82	Q9VW82 drosophila

17	14	28.0	9	11	O08979	mus musculus
18	14	28.0	10	2	Q47561	escherichia
19	14	28.0	10	2	Q60192	spiroplasma
20	14	28.0	10	2	Q93T35	acinetobact
21	14	28.0	10	3	Q9UW22	schizophyll
22	14	28.0	10	5	Q25355	locusta mig
23	14	28.0	10	6	Q9X884	equus cabal
24	14	28.0	10	6	Q95M70	trichosurus
25	14	28.0	10	6	Q9TR47	bos taurus
26	14	28.0	10	13	Q902V8	psittacus e
27	13	26.0	7	11	Q63480	rattus norv
28	13	26.0	8	4	Q9UMC7	homo sapien
29	13	26.0	8	8	Q34909	locusta mig
30	13	26.0	8	8	Q8WGC7	petrolisthe
31	13	26.0	8	12	Q83332	murine hepa
32	13	26.0	9	2	P83222	streptomyce
33	13	26.0	9	4	Q9UQA3	homo sapien
34	13	26.0	10	2	Q60194	spiroplasma
35	13	26.0	10	2	Q52837	rhizobium l
36	13	26.0	10	5	Q95NT8	musca domes
37	13	26.0	10	8	Q9ZYU4	scoloporus
38	13	26.0	10	8	Q9MJO5	podospira c
39	13	26.0	10	10	Q94IS6	pinus taeda
40	13	26.0	10	10	Q9S926	glycine max
41	13	26.0	10	10	Q9S936	beta vulgar
42	13	26.0	10	11	Q9QV21	rattus sp.
43	12	24.0	7	2	Q47505	escherichia
44	12	24.0	7	8	Q99182	gnatholebia
45	12	24.0	8	2	Q9AGP4	arthrobacte

ALIGNMENTS

RESULT 1

P82445 PRELIMINARY; PRT; 7 AA.

AC P82445; DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 10 kba cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=CV, PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed tobacco culture";
RL Planta 0:0-0(2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER
SQ SEQUENCE 7 AA; 758 MW; 69D2C1B862D1B2A0 CRC64;

Query Match 48.0%; Score 24; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 6.7e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VVRIGHLY 8
| :|:|:
Db 1 VTVGHVF 7

RESULT 2

Q14277 PRELIMINARY; PRT; 9 AA.

AC Q14277;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE RET protein short form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94071887; PubMed=7902707;
RA Ceccherini I., Boccardi R., Luo Y., Pasini B., Hofstra R.,
RA Takahashi M., Romeo G.;
RT "Exon structure and flanking intronic sequences of the human RET
RT proto-oncogene.";
RL Biochem. Biophys. Res. Commun. 196:1288-1295(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94366753; PubMed=8084609;
RA Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
RA Boccardi R., Nijveen H., Bollino A., Seri M., Ronchetto P., Pasini B.,
RA Bozzano M., Buys C., Romeo G.;
RT "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
RT the ret proto-oncogene.";
RL Oncogene 9:3025-3029(1994).
DR EMBL; U11532; AAC50102.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;

Query Match 38.0%; Score 19; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RIGLY 8
DB 1 RISHAF 6

RESULT 3
Q9YQ10 PRELIMINARY; PRT; 7 AA.
ID Q9YQ10
AC Q9YQ10; 7 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical fusion protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99099045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Piana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes.";
RL J. Virol. 73:1535-1545(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95159435; PubMed=7856095;
RA Eleouet J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.;
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1
RT of transmissible gastroenteritis virus.";
RL Virology 206:817-822(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88078100; PubMed=2825819;
RA Ragschaert D., Gelfi J., Laude H.;
RT "Phytic coronavirus TGEV: partial sequence of the genomic RNA its
RT organization and expression.";
RL Biochimie 69:591-600(1987).

DR EMBL; AJ011482; CAA09625.1; -.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 34.0%; Score 17; DB 12; Length 7;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 LYIL 10
DB 2 LYLL 5

RESULT 4
Q93SP2 PRELIMINARY; PRT; 8 AA.
ID Q93SP2
AC Q93SP2; 8 AA; 920 MW; FE2729C732C87336 CRC64;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Quaternary ammonium compound-resistance protein QacBdelta1
DE (Fragment).
GN QACBDELTA1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VMC704; TRANSDON=CLASS I INTEGRON;
RA Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
RT "VIM-2 metallo-beta-lactamase gene-containing integron in a
RT Pseudomonas aeruginosa clinical isolate.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029772; AAK50441.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 GHLYIL 10
DB 3 GVLFLL 8

RESULT 5
P83066 PRELIMINARY; PRT; 10 AA.
ID P83066
AC P83066; 10 AA; 11796; 11796; 11796; 11796; 11796; 11796; 11796; 11796; 11796;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
DE (Phosphohexokinase) (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE, AND INDUCTION.
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -1- CATALYTIC ACTIVITY: ATP + D-FRUCTOSE 6-PHOSPHATE = ADP + D-
CC FRUCTOSE 1,6-BISPHOSPHATE.
CC -1- PATHWAY: KEY CONTROL STEP OF GLYCOLYSIS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- INDUCTION: BY SALT STRESS.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOFRUCTOKINASE FAMILY.
DR InterPro; IPR000023; Pfufckinase.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; PARTIAL.
KW Kinase; transferase; Glycolysis.

```
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1061 MW; 6A9D98A732C87044 CRC64;

Query Match 32.0%; Score 16; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RIGHL 7
Db 3 RIGVL 7

RESULT 6
Q96Q19 ID Q96Q19 PRELIMINARY; PRT; 10 AA.
AC Q96Q19;
DT 01-DEC-2001 (TRENBLrel. 13, Created)
DT 01-DEC-2001 (TRENBLrel. 13, Last sequence update)
DE Mitochondrial ribosomal protein S30 (Fragment).
GN MRPS30.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429115; PubMed=11543634;
RA Kenmochi N., Suzuki T., Uechi T., Magoori M., Kuniba M., Higa S.,
RA Watanabe K., Tanaka T.;
RT "The human mitochondrial ribosomal protein genes: Mapping of 54 genes
RT to the chromosomes and implications for human disorders.";
RL Genomics 77:65-70(2001).
DR EMBL; AB061211; BAB54961.1; -.
KW Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1334 MW; C00B6751E44B0B46 CRC64;

Query Match 32.0%; Score 16; DB 4; Length 10;
Best Local Similarity 25.0%; Pred. No. 1.2e+04;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 HLYI 9
Db 7 HIFV 10

RESULT 7
Q9PXC3 ID Q9PXC3 PRELIMINARY; PRT; 10 AA.
AC Q9PXC3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE E antigen P20E (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE.
RX MEDLINE=92013147; PubMed=1717588;
RA Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
RA Ohnuma H., Tsuda F., Manekata E., Miyakawa Y., Mayumi M.;
RT "Molecular heterogeneity of e antigen polypeptides in sera from
RT carriers of hepatitis B virus.";
RL J. Immunol. 147:3156-3160(1991).
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1238 MW; 485A6E3AE721E9C7 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 10;
Best Local Similarity 22.2%; Pred. No. 1.2e+04;
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 2 VRIGHLYL 10
Db 1 MQLFHLXLI 9

RESULT 8
Q9XNP8 ID Q9XNP8 PRELIMINARY; PRT; 8 AA.
AC Q9XNP8;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE ATP synthase 6 (Fragment).
GN ATP6.
OS Boophilus microplus (Cattle tick).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N;
RX MEDLINE=99297341; PubMed=10368952;
RA Campbell N.J.H., Barker S.C.;
RT "The novel mitochondrial gene arrangement of the cattle tick,
RT Boophilus microplus: fivefold tandem repetition of a coding region.";
RL Mol. Biol. Evol. 16:732-740(1999).
DR EMBL; AF110616; AAD28386.1; -.
KW Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 938 MW; 58BB14404B5735B0 CRC64;

Query Match 30.0%; Score 15; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LYI 9
Db 3 LYI 5

RESULT 9
P83161 ID P83161 PRELIMINARY; PRT; 10 AA.
AC P83161;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE Putative RNA-binding protein rbpA (fragment).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxID=29412;
RN [1]
RP SEQUENCE.
RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
RL Submitted (OCT-2001) to the SWISS-PROT data bank.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
DR InterPro; IPR000504; RNA_rec_mot.
DR PROSITE; PS00030; RRM_RNP_1; PARTIAL.
KW RNA-binding.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1130 MW; 1DD09AB7244862DB CRC64;

Query Match 30.0%; Score 15; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.9e+04;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 VRIGHL 7
Db 2 IYVGNL 7
```

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RESULT 10
Q95NB1 PRELIMINARY; PRT; 10 AA.
AC Q95NB1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Malic enzyme (Fragment).
OS Eulemur fulvus (brown lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Eulemur.
OX NCBI_TaxID=13515;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., DeSalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
zone at Andringitra, Madagascar.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258167; AAK53147.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1075 MW; DD492B6D9D2C9D2 CRC64;

Query Match 30.0%; Score 15; DB 6; Length 10;
Best Local Similarity 25.0%; Pred. No. 1.9e+04;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 HLYI 9
DB [:::
2 HVFV 5

RESULT 11
Q95NB0 PRELIMINARY; PRT; 10 AA.
AC Q95NB0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Malic enzyme (Fragment).
OS Eulemur fulvus (brown lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Eulemur.
OX NCBI_TaxID=13515;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., DeSalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
zone at Andringitra, Madagascar.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258177; AAK53157.1; -.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1020 MW; DD492B6AFAF2C9D2 CRC64;

Query Match 30.0%; Score 15; DB 6; Length 10;
Best Local Similarity 25.0%; Pred. No. 1.9e+04;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 HLYI 9
DB [:::
2 HVFV 5

RESULT 12
P92762 PRELIMINARY; PRT; 10 AA.
AC P92762;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-MAY-2002 (TReMBLrel. 20, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COL.

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```

OS Uromastix acanthinura.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Uromastycinae;
OC Uromastix.
OX NCBI_TaxID=52167;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153826; PubMed=9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
RT "Two novel gene orders and the role of light-strand replication in
rearrangement of the vertebrate mitochondrial genome.";
RL Mol. Biol. Evol. 14:91-104(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97153820; PubMed=9000751;
RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT "Replication slippage may cause parallel evolution in the secondary
structures of mitochondrial transfer RNAs.";
RL Mol. Biol. Evol. 14:30-39(1997).
DR EMBL; U71325; AAC62249.1; -.
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1246 MW; DBD38E27336401ED CRC64;

Query Match 30.0%; Score 15; DB 8; Length 10;
Best Local Similarity 28.6%; Pred. No. 1.9e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 IGHLYL 10
DB [:::
2 MAHRWL 8

RESULT 13
Q05403 PRELIMINARY; PRT; 8 AA.
AC Q05403;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE DNA for ORF'S from chromosome XV (Fragment).
GN COQ3 AND VOL096C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=96021609; PubMed=8533473;
RA Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; X83121; CAA58183.1; -.
DR SGD; S0005456; COQ3.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 879 MW; 7B532D2D2C441E058 CRC64;

Query Match 28.0%; Score 14; DB 3; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVRI 4
DB [:::
5 VVKI 8

RESULT 14
Q47410 PRELIMINARY; PRT; 9 AA.
AC Q47410;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Pot. repAX peptide (Fragment).
 OS Escherichia coli.
 OG Plasmid NRI.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PLASMID NRI;
 RX MEDLINE=85160860; PubMed=2580099;
 RA Womble D.D., Sampathkumar P., Easton A.M., Luckow V.A., Rownd R.H.;
 RT "Transcription of the replication control region of the IncFII R-
 plasmid NRI in vitro and in vivo";
 RL J. Mol. Biol. 181:395-410(1985).
 DR EMBL; X02302; CAA26166.1; -.
 KW Plasmid.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1055 MW; DCFAG412CDDIE87D CRC64;

Query Match 28.0%; Score 14; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GH 6
 ||
 DB 3 GH 4

RESULT 15
 Q9H4M8
 ID Q9H4M8 PRELIMINARY; PRT; 9 AA.
 AC Q9H4M8;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
 DE PAR2 (Fragment).
 GN NRII2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PERIPHERAL BLOOD;
 RA Pentecost B.F., Ling G.;
 RT "The human pregnane X receptor promoter complex provides
 transcriptional starts for a number of pXR related transcripts.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY007189; AAG23345.1; -.
 FT NON_TER
 SQ SEQUENCE 9 AA; 1129 MW; 82F8E1F1B411B2D1 CRC64;

Query Match 28.0%; Score 14; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VVRIGH 6
 | | |
 DB 3 VTRTHH 8

Search completed: December 19, 2002, 16:51:41
 Job time : 59 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:55:35 : Search time 15 Seconds
(without alignments)
51.272 Million cell updates/sec

Title: US-09-692-401-6

Perfect score: 42

Sequence: 1 RIGHLYL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 604

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	17	40.5	4	2 I38888	COI intron 16 prot
2	15	35.7	4	2 PLO140	carbon-monoxide de
3	14	33.3	3	3 GKHO	growth-modulating
4	14	33.3	6	2 A61419	sarcosine dehydrog
5	14	33.3	6	2 B56979	collagen alpha 1(I
6	14	33.3	7	1 NYPG7	hypothalamic hepta
7	14	33.3	7	2 S42407	gramicidin S synth
8	14	33.3	7	2 A28709	phosphonoacetaldeh
9	14	33.3	8	2 A61467	penalbumin - Adeli
10	13	31.0	4	2 PT0721	T-cell receptor be
11	13	31.0	7	2 A60139	fatty-acid synthas
12	13	31.0	7	2 PQ0663	membrane protein -
13	13	31.0	7	2 A25269	sex pheromone cAM3
14	13	31.0	7	4 I56695	hypothetical L2 pr
15	12	28.6	4	2 A48360	gamma subunit of p
16	12	28.6	6	2 A60986	N-formyl oligopept
17	12	28.6	8	2 B45800	serum albumin - do
18	12	28.6	8	2 PC4373	telomeric and tetr
19	11	26.2	5	2 PQ0009	angiotensin-conver
20	11	26.2	5	3 JT0870	phytoalkifone alp
21	11	26.2	7	2 S71867	glutathione transp
22	11	26.2	7	2 S08606	hypothetical prote
23	11	26.2	7	2 S45311	microcin C7 - Esch
24	11	26.2	7	2 A11483	aspartate transami
25	11	26.2	7	2 S58797	serine/threonine-s
26	11	26.2	7	2 S33567	tubulin beta-3 cha
27	11	26.2	8	2 S66646	cardioacceleratory
28	11	26.2	8	2 PH1618	Ig H chain V-D-J r
29	11	26.2	8	2 PN0043	phosphatidylethano

30	11	26.2	8	2 PC4372	telomeric and tetr
31	11	26.2	8	2 T13818	cytochrome oxidase
32	10	23.8	5	2 F22565	R-phycoerythrin ga
33	10	23.8	5	2 S53595	hypothetical prote
34	10	23.8	6	2 I37263	Y protein - human
35	10	23.8	6	2 PT0662	T-cell receptor be
36	10	23.8	6	2 A43129	neuropeptide GNTFR
37	10	23.8	7	2 S71870	glutathione transp
38	10	23.8	7	2 A38081	amine oxidase (cop
39	10	23.8	7	2 T09512	NADH2 dehydrogenas
40	10	23.8	8	2 A31570	angiotensin-conver
41	10	23.8	8	2 S19288	acylase - Kluyvera
42	10	23.8	8	2 PT0368	Ig gamma chain C r
43	10	23.8	8	2 A54823	olfactory receptor
44	10	23.8	8	2 PT0691	T-cell receptor be
45	10	23.8	8	2 B54823	olfactory receptor

ALIGNMENTS

RESULT 1

I38888

COI intron 16 protein - Podospora anserina mitochondrion

C:Species: mitochondrion Podospora anserina

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-Dec-1999

C:Accession: I38888

C:Cur. Genet. 16, 381-406, 1989

A:Title: DNA sequence analysis of the 24.5 kilobase pair cytochrome oxidase subunit

A:Reference number: A48327; MUID:90124722; PMID:2558809

A:Accession: I38888

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-4 <CUM>

A:Cross-references: GB:X55026; GB:M30937; GB:M61734

C:Genetics:

A:Genome: mitochondrion

A:Genetic code: SGC3

C:Keywords: mitochondrion

Query Match 40.5%; Score 17; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIGH 4
DB 1 QLGH 4

RESULT 2

PL0140

Carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrog

C:Species: Pseudomonas carboxydohydrogena

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993

C:Accession: PL0140

C:Cur. Genet. 152, 335-341, 1989

A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydo

A:Reference number: PL0138; MUID:90055678; PMID:2818128

A:Accession: PL0140

A:Molecule type: protein

A:Residues: 1-4 <KRA>

C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large,

C:Keywords: oxidoreductase

Query Match 35.7%; Score 15; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGH 4
DB 1 MGH 3

RESULT 3
GKHU
growth-modulating peptide - human
C:Species: Homo sapiens (man)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A01421
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A:Reference number: A01421; MUID:77162369; PMID:856356
A:Accession: A01421
A:Molecule type: protein
A:Residues: 1-3 <SCH>
A>Note: This serum tripeptide is found to stimulate growth of some cell types and to inhibit tumor growth.
C:Superfamily: unassigned animal peptides

Query Match 33.3%; Score 14; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4
DB 1 GH 2

RESULT 4
A61419
sarcosine dehydrogenase (EC 1.5.99.1) - Pseudomonas sp. (strain WRF) (fragment)
C:Species: Pseudomonas sp.
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C:Accession: A61419
R:Pinto, J.T.; Frisell, W.R.
Arch. Biochem. Biophys. 169, 483-491, 1975
A:Title: Characterization of the peptide-bound flavin of a bacterial sarcosine dehydrogenase.
A:Reference number: A61419; MUID:76038634; PMID:241294
A:Accession: A61419
A:Molecule type: protein
A:Residues: 1-6 <PIN>
C:Keywords: FAD; flavoprotein; oxidoreductase; phosphoprotein
F:6/Modified site: 3'-FAD-histidine (His) #status experimental

Query Match 33.3%; Score 14; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4
DB 5 GH 6

RESULT 5
B56979
collagen alpha 1(II) chain - bovine (fragment)
N:Alternate names: collagen alpha 3(XI) chain
C:Species: Bos primigenius taurus (cattle)
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C:Accession: B56979
R:Wu, J.J.; Eyre, D.R.
J. Biol. Chem. 270, 18865-18870, 1995
A:Title: Structural analysis of cross-linking domains in cartilage type XI collagen. In situ cross-linking of collagen type XI.
A:Reference number: A56978; MUID:95370194; PMID:7642541
A:Accession: B56979
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-6 <WUA>
A>Note: the residue designated "X" is modified lysine in collagen 1(II) some cross-linked

Query Match 33.3%; Score 14; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4
DB 4 GH 5

RESULT 6
NYPG7
hypothalamic heptapeptide - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 23-Aug-1996
C:Accession: A01417
R:Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kon
Horm. Metab. Res. 13, 228-232, 1981
A:Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-rele
A:Reference number: A01417; MUID:81213980; PMID:6263778
A:Accession: A01417
A:Molecule type: protein
A:Residues: 1-7 <CHA>
C:Superfamily: hypothalamic heptapeptide
C:Keywords: hypothalamus

Query Match 33.3%; Score 14; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IGHLY 6
DB 2 IYHSY 6

RESULT 7
S42407
gramicidin S synthetase component II - Bacillus brevis (fragment)
C:Species: Bacillus brevis
C>Date: 20-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 12-Apr-1996
C:Accession: S42407
R:Stein, T.; Vater, J.; Kruff, V.; Wittmann-Liebold, B.; Franke, P.; Panico, M.; Mc D
FEBS Lett. 340, 39-44, 1994
A:Title: Detection of 4'-phosphopantetheine at the thioester binding site for L-valin
A:Reference number: S42407; MUID:94164305; PMID:8119405
A:Accession: S42407
A:Molecule type: protein
A:Residues: 1-7 <STE>

Query Match 33.3%; Score 14; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4
DB 3 GH 4

RESULT 8
A28709
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C:Species: Bacillus cereus
C>Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C:Accession: A28709
R:Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A:Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Eviden
due.
A:Reference number: A28709; MUID:88241058; PMID:3132206
A:Accession: A28709
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <OLS>

Query Match 33.3%; Score 14; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIGHL 5
:| |:
Db 2 KIDHV 6

RESULT 9
A61467
penalbumin - Adelle penguin (fragment)
C:Species: Pygoscelis adelle (Adelle penguin)
C:Date: 07-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 04-Nov-1994
C:Accession: A61467
R:Osuga, D.T.; Aminlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.E.
J. Protein Chem. 2, 43-62, 1983
A:Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparisons
A:Reference number: A61467
A:Accession: A61467
A:Molecule type: protein
A:Residues: 1-8 <OSU>
C:Comment: Penalbumin is a major protein component of egg whites from penguins but not f
C:Keywords: egg white; glycoprotein

Query Match 33.3%; Score 14; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GHLY 6
:| |:
Db 1 GSIY 4

RESULT 10
PT0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0721
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0721
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FEE>
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.0%; Score 13; DB 2; Length 4;
Best Local Similarity 56.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIG 3
:| |:
Db 2 RLG 4

RESULT 11
A60139
fatty acid synthase (EC 2.3.1.85) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 26-May-2000
C:Accession: A60139
R:Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.
Biochim. Biophys. Acta 828, 380-382, 1985
A:Title: Amino acid sequence around the reactive serine residue of the thioesterase doma
A:Reference number: A60139; MUID:85175165; PMID:3921056
A:Accession: A60139
A:Molecule type: protein
A:Residues: 1-7 <HAR>
C:Superfamily: rat fatty acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I hom
C:Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional en
F:5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 31.0%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GHLY 6
:| |:
Db 3 GYSY 6

RESULT 12
PQ0663
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C:Species: porcine epidemic diarrhea virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C:Accession: PQ0663
R:Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epid-
A:Reference number: JQ2191; MUID:93389433; PMID:8397280
A:Accession: PQ0663
A:Molecule type: mRNA
A:Residues: 1-7 <BRI>
A:Cross-references: GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:g584083
C:Comment: This virus is coronavirus related to human coronavirus 229E.
C:Keywords: membrane protein

Query Match 31.0%; Score 13; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIGHL 5
:| |:
Db 2 KVLHL 6

RESULT 13
A25269
sex pheromone cAM373 - Enterococcus faecalis
N:Alternate names: clumping-inducing agent (CIA)
C:Species: Enterococcus faecalis
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993
C:Accession: A25269
R:Mori, M.; Tanaka, H.; Sakagami, Y.; Isogai, A.; Fujino, M.; Kitada, C.; White, B.A
FEBS Lett. 206, 69-72, 1986
A:Title: Isolation and structure of the Streptococcus faecalis sex pheromone, cAM373
A:Reference number: A25269; MUID:87005252; PMID:3093276
A:Accession: A25269
A:Molecule type: protein
A:Residues: 1-7 <MOR>

Query Match 31.0%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVIL 8
:| |:
Db 2 IFIL 5

RESULT 14
I56695
hypothetical L2 protein (mistranslated) - human papillomavirus type 16 (fragment)
C:Species: human papillomavirus type 16
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: I56695
R:Schneider-Maunoury, S.; Croissant, O.; Orth, G.
J. Virol. 61, 3295-3298, 1987
A:Title: Integration of human papillomavirus type 16 DNA sequences: a possible early
A:Reference number: I56695; MUID:87311896; PMID:3041049
A:Accession: I56695
A:Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-7 <SCH>
C;Cross-references: GB:M30709; NID:g190253; PIDN:AAA65995.1; PID:g553616
A;Comment: This is the hypothetical translation of a viral sequence integrated into the
C;Comment: It is translated in an incorrect, -1, reading frame of the L2 protein.

Query Match 31.0%; Score 13; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 HLY 6
| |
Db 1 HSY 3

RESULT 15
A48360
gamma subunit of Protein A - Methylosinus trichosporium (fragment)
C;Species: Methylosinus trichosporium
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A48360
R;Cardy, D.L.; Laidler, V.; Salmond, G.P.; Murrell, J.C.
Arch. Microbiol. 156, 477-483, 1991
A;Title: The methane monooxygenase gene cluster of Methylosinus trichosporium: cloning a
A;Reference number: A48360; MUID:92153031; PMID:1785954
A;Contents: OB3b
A;Accession: A48360
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4 <CAR>
A;Cross-references: GB:S81887; NID:g245213; PIDN:AA821391.1; PID:g245214
A;Note: sequence extracted from NCBI backbone (NCBI:81887, NCBIP:81912)

Query Match 28.6%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 HL 5
| |
Db 1 HL 2

Search completed: December 19, 2002, 16:58:00
Job time : 16 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:52:44 ; Search time 10 seconds
(without alignments)
33.181 Million cell updates/sec

Title: US-09-692-401-6
Perfect score: 42
Sequence: 1 RIGHLYIL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 150

Minimum DB seq length: 0
Maximum DB seq length: 8

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	15	35.7	4	DCML_PSECH	P19916 pseudomonas
2	14	33.3	3	GRWM_HUMAN	P01157 homo sapien
3	14	33.3	7	FAR2_ASCSU	P31890 ascaris suu
4	14	33.3	7	HY7_PIG	P01153 sus scrofa
5	13	31.0	7	CIA_ENTFA	P11932 enterococu
6	13	31.0	7	GFRP_MOUSE	P99025 mus musculu
7	12	28.6	8	ANG2_BOTJA	Q10582 bothrops ja
8	11	26.2	5	FARP_ARTTR	P41853 artiopesthi
9	11	26.2	5	PSK_DAUCA	P58261 daucus caro
10	11	26.2	7	UN06_PINPS	P81675 pinus pinas
11	11	26.2	8	ALI6_CYPDO	P82157 cydia pomon
12	10	23.8	5	TPIS_CANFA	P54714 canis famil
13	10	23.8	5	UF01_MOUSE	P38639 mus musculu
14	10	23.8	6	FARP_MONEX	P41966 moniezia ex
15	10	23.8	7	FAR5_HIRME	P42564 hirudo medi
16	10	23.8	8	ACI_THUAL	P18691 thunnus alb
17	10	23.8	8	UF06_MOUSE	P38644 mus musculu
18	9	21.4	4	EOSI_HUMAN	P02731 homo sapien
19	9	21.4	4	FAR3_HIRME	P42562 hirudo medi
20	9	21.4	4	EYRI_ANFEL	P58706 anthopleura
21	9	21.4	5	BI0B_CITFR	P12997 citrobacter
22	9	21.4	5	PRCT_PERAM	F01373 periplaneta
23	9	21.4	5	RE32_LITRU	P82073 litoria rub
24	9	21.4	6	TRPI_PSEPU	P36414 pseudomonas
25	9	21.4	7	ALL7_CYPDO	P82158 cydia pomon
26	9	21.4	7	EI05_LITRU	P82101 litoria rub
27	9	21.4	8	AL12_CARMA	P81815 carcinus ma
28	9	21.4	8	AL18_CARMA	P81821 carcinus ma
29	9	21.4	8	CAD1_ENTFA	P13268 enterococu
30	9	21.4	8	FAR7_ASCSU	P43171 ascaris suu
31	9	21.4	8	FUSS_FUSSO	P81010 fusarium so
32	8	19.0	3	THYL_PIG	P01151 sus scrofa
33	8	19.0	4	FAR4_HIRME	P42563 hirudo medi

34	8	19.0	5	1	EI03_LITRU	P82099 litoria rub
35	8	19.0	5	1	EI04_LITRU	P82100 litoria rub
36	8	19.0	5	1	PAP2_PARMA	P81864 pardachirus
37	8	19.0	6	1	CIP1_MYTED	P13736 mytilus edu
38	8	19.0	6	1	CIP2_MYTED	P13737 mytilus edu
39	8	19.0	6	1	TMOF_SARBU	P41495 sarcophaga
40	8	19.0	7	1	CHOX_AICSP	P81298 haemochnus
41	8	19.0	7	1	FAR3_HAECO	P41874 panagrellus
42	8	19.0	7	1	FAR3_PANRE	P42984 leptinotars
43	8	19.0	7	1	MNPI_LBPDE	P82065 litoria rub
44	8	19.0	7	1	TY51_LITRU	P38641 mus musculu
45	8	19.0	7	1	UF03_MOUSE	

ALIGNMENTS

RESULT 1
DCML_PSECH STANDARD; PRT; 4 AA.
ID P19916;
AC 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTL.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydohydrogenic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -!- COFACTOR: Molybdenum (molybdopterin).
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
CC PIR; P10140; P10140.
CC Oxidoreductase; Molybdenum.
FT NON_TER 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 35.7% ; Score 15; DB 1; Length 4;
Best Local Similarity 66.7% ; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 IGH 4
Db 1 MGH 3

RESULT 2
GRWM_HUMAN STANDARD; PRT; 3 AA.
ID P01157;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.

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RX MEDLINE=77162369; PubMed=958356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
RC -1- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR PIR; A01421; GKHU.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 33.3%; Score 14; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GH 4
   ||
DB 1 GH 2

RESULT 3
FAR2_ASCSU STANDARD; PRT; 7 AA.
ID FAR2_ASCSU
AC F31890;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF2.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
NCBI_TaxID=6253, 6233;
[1]
RN
RP SEQUENCE.
RC SPECIES=A.suum;
RX MEDLINE=93324431; PubMed=8332542;
RA Cowden C., Stretton A.O.W.;
RT "AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
RL Peptides 14:423-430(1993).
RN
RP SEQUENCE.
RC SPECIES=P.redivivus;
RX MEDLINE=95060998; PubMed=7970891;
RA Maule A.G., Shaw C., Bowman J.W.;
RT "The FMRamide-like neuropeptide AF2 (Ascaris suum) is present in the
RL free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida).";
RC Parasitology 109:351-356(1994).
CC -1- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.
CC -1- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide; Amidation.
KW MOD_RES 7
FT SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;
SQ

Query Match 33.3%; Score 14; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9823;
RP	[1]
RP	SEQUENCE, AND SYNTHESIS.
RX	MEDLINE=81213980; PubMed=6263778;
RX	Chang R.C.C., Huang W.-Y., Arimura A., Redding T.W., Coy D.H.,
RA	Saffran M., Kong A., Hamilton J.W., Cohn D.V., Schally A.V.;
RT	"Isolation, structure and synthesis of a heptapeptide with in vitro
RT	ACTH-releasing activity from porcine hypothalamus.";
RL	Horm. Metab. Res. 13:228-232(1981).
DR	PIR; A01417; NYP67
SQ	SEQUENCE 7 AA; 957 MW; 632B45B1FB5059A0 CRC64;
Query Match 33.3%; Score 14; DB 1; Length 7;	
Best Local Similarity 60.0%; Pred. No. 1.1e+05;	
Matches	3; Conservative 0; Mismatches 2; Indels 0; Gaps
QY	2 IGHLY 6
DB	2 IYHSY 6
[1]	
RESULT 5	
CIA_ENTFA	
ID	CIA_ENTFA STANDARD; PRT; 7 AA.
AC	PI1932;
DT	01-OCT-1989 (Rel. 12, Created)
DT	01-OCT-1989 (Rel. 12, Last sequence update)
DT	01-FEB-1991 (Rel. 17, Last annotation update)
DE	Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS	Enterococcus faecalis [Streptococcus faecalis]
OS	Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus
OX	NCBI_TaxID=1351;
RP	[1]
RP	SEQUENCE.
RX	MEDLINE=87005252; PubMed=3093276;
RX	Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA	White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT	"Isolation and structure of the Streptococcus faecalis sex pheromone
RT	CAM373.";
RL	FEBS Lett. 206:69-72(1986).
DR	PIR; A25269; A25269.
KW	Pheromone.
SQ	SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
Query Match 31.0%; Score 13; DB 1; Length 7;	
Best Local Similarity 50.0%; Pred. No. 1.1e+05;	
Matches	2; Conservative 2; Mismatches 0; Indels 0; Gaps
QY	5 LYIL 8
DB	2 IFIL 5
[1]	
RESULT 6	
GFRP_MOUSE	
ID	GFRP_MOUSE STANDARD; PRT; 7 AA.
AC	P99025;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	GPR cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN	GCHFR OR GFRP.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;

```
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA Cowthorne M.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
CC !- FUNCTION: MEDIATES TETRAHYDROBIOTERIN INHIBITION OF GTP
CC CYCLOHYDROLASE 1. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
CC (BY SIMILARITY).
CC !- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC SWISS-PROT: P99025; MOUSE.
FT INIT_MET 0
FT NON_TER 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;

Query Match 31.0%; Score 13; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 YIL 8
DB 2 YIL 4

RESULT 7
ANG2_BOTJA
ID ANG2_BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca.";
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC !- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 28.6%; Score 12; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LYI 7
DB 3 VII 5

RESULT 8
FARP_ARTTR
ID FARP_ARTTR STANDARD; PRT; 5 AA.
AC P41853;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide RYIRF-amide.
OS Artoposthia triangulata.
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC Terricola; Geoplanidae; Arthurdendyus.

OX NCBI_TaxID=132421;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=94211927; PubMed=7909164;
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
RT "RYIRFamide: a turbellarian FMRamide-related peptide (FARP).";
RL Regul. Pept. 50:37-43(1994).
CC !- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 5
FT SEQUENCE 5 AA; 754 MW; 69D4004B4600000 CRC64;

Query Match 26.2%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YI 7
DB 2 YI 3

RESULT 9
PSK_DAUCA
ID PSK_DAUCA STANDARD; PRT; 5 AA.
AC P58261;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phytosulfokine-alpha (PSK-alpha) [Contains: Phytosulfokine-beta (PSK-beta)].
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE, AND IDENTIFICATION BY MASS SPECTROMETRY.
RC STRAIN=cv. US-Harunakigosun;
RX MEDLINE=20212743; PubMed=10750705;
RA Hanai H., Matsuno T., Yamamoto M., Matsubayashi Y., Kobayashi T.,
RA Kamada H., Sakagami Y.;
RT "A secreted peptide growth factor, phytosulfokine, acting as a
RT stimulatory factor of carrot somatic embryo formation.";
RL Plant Cell Physiol. 41:27-32(2000).
CC !- FUNCTION: IN PRESENCE OF 2,4-D, STIMULATES PROLIFERATION OF THE
CC CELLS, BUT DOES NOT STIMULATE DIFFERENTIATION INTO THE SOMATIC
CC EMBRYOS.
CC !- SUBCELLULAR LOCATION: Secreted.
CC !- PTM: SULFATION IS IMPORTANT FOR ACTIVITY AND FOR THE BINDING TO A
CC PUTATIVE MEMBRANE RECEPTOR (BY SIMILARITY).
CC !- SIMILARITY: BELONGS TO THE PHYTOSULFOKINE FAMILY.
KW Growth factor; Sulfation.
FT PEPTIDE 1 4
FT MOD_RES 1 1
FT MOD_RES 3 3
FT SEQUENCE 5 AA; 687 MW; 76C1B504B300000 CRC64;

Query Match 26.2%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YI 7
DB 1 YI 2

RESULT 10
UN06_PINPS
ID UN06_PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
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DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 Kda.
FT NON_TER 1 1
FT SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 26.2%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LY 6
DB 1 LY 2

RESULT 11
ALL6_CYPDO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
OC Ditrysia; Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
FT SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 26.2%; Score 11; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LY 6
DB 3 LY 4

RESULT 12
TPIS_CANFA STANDARD; PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).

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GN TP11.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycero-
CC phosphate.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR HSC-2DPAGE; P54714; DOG.
DR InterPro; IPR000652; Triophos_ismrse.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 23.8%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGH 4
DB 2 VGN 4

RESULT 13
UF01_MOUSE STANDARD; PRT; 5 AA.
ID UF01_MOUSE
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 Kda.
FT NON_TER 5 5
FT SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 23.8%; Score 10; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IG 3
DB 2 IG 3

RESULT 14
FARP_MONEX STANDARD; PRT; 6 AA.
ID FARP_MONEX

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AC P41966;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FMRFamide-like neuropeptide GNFRF-amide.
OS Moniezia expansa (Sheep tapeworm).
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Anoplocephalidae; Moniezia.
OX NCBI_TaxID=28841;
RN [1]
RP SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G., Shaw C., Halton D.W., Thim L.;
RT "GNFRFamide: a novel FMRFamide-immunoreactive peptide isolated from
RL the sheep tapeworm, Moniezia expansa.";
RL Biochem. Biophys. Res. Commun. 193:1054-1060(1993).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 787 MW; 69D409C9C4481000 CRC64;

Query Match 23.8%; Score 10; DB 1; Length 6;
Best Local Similarity 25.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GHLY 6
DB 1 GNFF 4

RESULT 15
FARS_HIRME STANDARD; PRT; 7 AA.
AC P42564;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide GGYMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;

Query Match 23.8%; Score 10; DB 1; Length 7;
Best Local Similarity 40.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 GHLYI 7
DB 1 GGYM 5

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Search completed: December 19, 2002, 16:56:50
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:54:55 ; Search time 42 seconds

(without alignments)
39.247 Million cell updates/sec

Title: us-09-692-401-6

Perfect score: 42

Sequence: 1 RIGHLYIL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 390

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.Ordanelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	50.0	7	10	P82445 nicotiana t
2	17	40.5	7	12	Q9YQ10 transmissib
3	16	38.1	8	2	Q93SP2 pseudomonas
4	15	35.7	8	8	Q9XNP8 boophilus m
5	13	31.0	8	4	Q9UMC7 homo sapien
6	13	31.0	8	8	Q8WGC7 petrolisthe
7	13	31.0	8	12	Q83332 murine hepa
8	12	28.6	7	8	Q9182 gnatholebia
9	12	28.6	8	2	Q9AGP4 arthrobacte
10	12	28.6	8	6	Q9XSV1 canis famil
11	11	26.2	7	2	Q47505 escherichia
12	11	26.2	8	2	Q9RQ57 buchnera ap
13	11	26.2	8	2	Q9RQ49 buchnera ap
14	11	26.2	8	2	Q9R7T2 escherichia
15	11	26.2	8	4	Q9UHK1 homo sapien
16	11	26.2	8	4	Q9UDZ4 homo sapien

17	11	26.2	8	4	Q9BY5	homo sapien
18	11	26.2	8	6	O02831	oryctolagus
19	11	26.2	8	6	Q9BFC3	didelphis m
20	11	26.2	8	6	Q9BFC2	macropus eu
21	11	26.2	8	6	Q9BFC1	choloepus h
22	11	26.2	8	6	Q9BFC0	choloepus d
23	11	26.2	8	6	Q9BF99	euphractus
24	11	26.2	8	6	Q9BF98	chaetophrac
25	11	26.2	8	6	Q9BF97	tamandua te
26	11	26.2	8	6	Q9BF96	myimecophag
27	11	26.2	8	6	Q9BF95	erimaceus c
28	11	26.2	8	6	Q9BF94	taipa alta
29	11	26.2	8	6	Q9BF93	condylura c
30	11	26.2	8	6	Q9BF92	sorex arane
31	11	26.2	8	6	Q9BF91	echinops te
32	11	26.2	8	6	Q9BF90	trichechus
33	11	26.2	8	6	Q9BF89	procavia ca
34	11	26.2	8	6	Q9BF88	loxodonta a
35	11	26.2	8	6	Q9BF87	macroscelid
36	11	26.2	8	6	Q9BF86	orycteropus
37	11	26.2	8	6	Q9BF85	cynocephalu
38	11	26.2	8	6	Q9BF84	tupaia mno
39	11	26.2	8	6	Q9BF83	lemur catta
40	11	26.2	8	6	Q9BF82	tarsius ban
41	11	26.2	8	6	Q9BF81	ateles fusc
42	11	26.2	8	6	Q9BF80	macaca mula
43	11	26.2	8	6	Q9BF99	hylobates c
44	11	26.2	8	6	Q9BF98	callimico g
45	11	26.2	8	6	Q9BF97	artibeus ja

ALIGNMENTS

RESULT 1

P82445 PRELIMINARY: PRT: 7 AA.
AC P82445;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 10 kDa cell wall protein (fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture";
RL Planta 0.0-0(2000);
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER
SQ SEQUENCE 7 AA: 758 MW; 69D2CIE8G2DIB2A0 CRC64;
Query Match 50.0%; Score 21; DB 10; Length 7;
Best Local Similarity 40.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Query Match

Score 21; DB 10; Length 7;

Best Local Similarity 40.0%; Pred. No. 6.7e+05;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGHLY 6

Db 3 VGRVF 7

!!!:

RESULT 2

Q9YQ10

ID Q9YQ10 PRELIMINARY: PRT: 7 AA.

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AC O9YQ10;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical fusion protein.
OS Transmissible gastroenteritis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11149;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9909045; PubMed=9882359;
RA Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
RA Enjuanes L.;
RT "Replication and packaging of transmissible gastroenteritis
RT coronavirus-derived synthetic minigenomes.";
RL J. Virol. 73:1535-1545(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95159435; PubMed=7856095;
RA Eleuet J., Raschaert D., Lambert P., Levy L., Vende P., Laude H.;
RT "Complete sequence (20 kilobases) of the polyprotein-encoding gene 1
RT of transmissible gastroenteritis virus.";
RL Virology 206:817-822(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88078100; PubMed=2825819;
RA Raschaert D., Geif J., Laude H.;
RT "Enteric coronavirus TGEV: partial sequence of the genomic RNA its
RT organization and expression.";
RL Biochimie 69:591-600(1987).
DR EMBL; AJ011482; CAA09625.1; -.
SQ SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;

Query Match 40.5%; Score 17; DB 12; Length 7;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVYL 8
DB 2 LVLL 5

RESULT 3
Q93SP2 ID Q93SP2 PRELIMINARY; PRT; 8 AA.
AC Q93SP2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Quaternary ammonium compound-resistance protein Qacsdelta1
DE (Fragment).
GN QACDELTA1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMC704; TRANSPOSON-CLASS I INTEGRON;
RA Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
RT "VIM-2 metallo-beta-lactamase gene-containing integron in a
RT Pseudomonas aeruginosa clinical isolate.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029772; AAK50441.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

Query Match 38.1%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GHLYL 8

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DB 3 GVLELL 8

RESULT 4
Q9XNP8 ID Q9XNP8 PRELIMINARY; PRT; 8 AA.
AC Q9XNP8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE ATP synthase 6 (Fragment).
GN ATP6.
OS Bophilius microplus (Cattle tick).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=6541;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N;
RX MEDLINE=99297341; PubMed=10368952;
RA Campbell N.J.H., Barker S.C.;
RT "The novel mitochondrial gene arrangement of the cattle tick,
RT Bophilius microplus: fivefold tandem repetition of a coding region.";
RL Mol. Biol. Evol. 16:732-740(1999).
DR EMBL; AF110616; AAD28386.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 8 AA; 938 MW; 58BB14404B5735B0 CRC64;

Query Match 35.7%; Score 15; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LYI 7
DB 3 LYI 5

RESULT 5
Q9UMC7 ID Q9UMC7 PRELIMINARY; PRT; 8 AA.
AC Q9UMC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE SHMT protein (Fragment).
GN SHMT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Chave K.J., Snell K., Sanders P.G.;
RT "Isolation and characterisation of human genomic sequences encoding
RT cytosolic serine hydroxymethyltransferase.";
RL Biochem. Soc. Trans. 25:53-53(1997).
DR EMBL; Y14492; CAB54844.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 868 MW; 7C205721E44AB5B8 CRC64;

Query Match 31.0%; Score 13; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HLYI 7
DB 5 HLLI 8

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RESULT 6
O8WGC7 PRELIMINARY; PRT; 8 AA.
AC O8WGC7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
OS Petrolisthes armatus (green porcelain crab).
OC Mitochondrion.
CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura;
CC Galatheoidea; Porcellanidae; Petrolisthes.
OX NCBI_TaxID=84662;
RN [1]
RP SEQUENCE FROM N.A.
RA Morrison C.L., Harvey A.W., Lavery S., Tieu K., Huang Y.,
RA Cunningham C.W.;
RT "Mitochondrial gene rearrangements support a hypothesis of parallel
RT evolution to the crab-like form.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF436049; AAL31623.1; -.
KW Mitochondrion.
FT NON_TER 8
FT SEQUENCE 8 AA; 1010 MW; FE20504B54472696 CRC64;
Query Match 31.0%; Score 13; DB 8; Length 8;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 YIL 8
Db 5 YII 7

RESULT 7
O83332 PRELIMINARY; PRT; 8 AA.
AC O83332;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hemagglutinin-esterase (Fragment).
OS murine hepatitis virus.
CC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
CC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11138;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-JHM;
RX MEDLINE=95191005; PubMed=7884877;
RA Kim K.H., Makino S.;
RT "Two murine coronavirus genes suffice for viral RNA synthesis.";
RL J. Virol. 69:2313-2321(1995).
DR EMBL; U19933; AAA69002.1; -.
FT NON_TER 1
FT NON_TER 8
FT SEQUENCE 8 AA; 907 MW; 92273B5B1735A2CD CRC64;
Query Match 31.0%; Score 13; DB 12; Length 8;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 6 YIL 8
Db 6 YII 8

RESULT 8
O99182 PRELIMINARY; PRT; 7 AA.
AC O99182;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

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DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN COL.
OS Gnatholebias zonatus.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX NCBI_TaxID=135316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20072928; PubMed=10603257;
RA Murphy W.J., Thomson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002591; AAD01074.1; -.
KW Mitochondrion.
FT NON_TER 1
FT SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;
Query Match 28.6%; Score 12; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 HL 5
Db 5 HL 6

RESULT 9
Q9AGB4 PRELIMINARY; PRT; 8 AA.
AC Q9AGB4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Serine hydroxymethyltransferase (Fragment).
GN GLYA.
OS Arthrobacter sp. LIN.
CC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
CC Actinomycetales; Micrococcales; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=153502;
RN [1]
RP SEQUENCE FROM N.A.
RA Meskys R., Harris R.J., Casalte V., Bastran J., Scrutton N.S.;
RT "Genetic organization of the genes involved in dimethylglycine and
RT sarcosine degradation in Arthrobacter spp.: implications for glycine
RT betaine catabolism.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF328478; AAK16486.1; -.
KW Methyltransferase; Transferase.
FT NON_TER 1
FT SEQUENCE 8 AA; 898 MW; 6B18705333372457 CRC64;
Query Match 28.6%; Score 12; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIG 3
Db 5 RIG 7

RESULT 10
Q9XSV1 PRELIMINARY; PRT; 8 AA.
AC Q9XSV1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

```

```
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Retinoblastoma protein (Fragment).
GN RBL
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97049323; PubMed=8894053;
RA Venter P.J.; Brucillette J.A.; Yuzbasyan-Gurkan V.; Brewer G.J.;
RT "Gene-specific universal mammalian sequence-tagged sites: application
to the canine genome."
RL Biochem. Genet. 34:321-341(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Venter P.J.; Cao Y.; Alexander L.; Yuzbasyan-Gurkan V.;
RT "Dinucleotide repeat polymorphism in the canine retinoblastoma (RBL)
gene."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF155737; AAD38807.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 895 MW; 1425BB18676721E3 CRC64;

Query Match 28.6%; Score 12; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HL 5
DB 2 HL 3

RESULT 11
ID Q47505 PRELIMINARY; PRT; 7 AA.
AC Q47505;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MCCA protein.
GN MCCA.
OS Escherichia coli.
OG Plasmid pMCC7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96099297; PubMed=8522520;
RA Gonzalez-Pastor J.E.; San Millan J.L.; Castilla M.A.; Moreno F.;
RT "Structure and organization of plasmid genes required to produce the
translational inhibitor microcin C7."
RL J. Bacteriol. 177:7131-7140(1995).
DR EMBL; X57583; CAA40808.1; -.
KW Plasmid.
SQ SEQUENCE 7 AA; 763 MW; 644DD44861B406F0 CRC64;

Query Match 26.2%; Score 11; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIGH 4
DB 2 RTGN 5

RESULT 12
ID Q9RQ57 PRELIMINARY; PRT; 8 AA.
AC Q9RQ57;
```

```
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Nifs protein homolog (Fragment).
GN NIFS.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022990; PubMed=10555290;
RA Clark M.A.; Moran N.A.; Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
compositions."
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL; AF130812; AAF13797.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 980 MW; F3A73B504771A336 CRC64;

Query Match 26.2%; Score 11; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 6.7e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LYI 7
DB 5 IYL 7

RESULT 13
ID Q9RQ49 PRELIMINARY; PRT; 8 AA.
AC Q9RQ49;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Nifs protein homolog (Fragment).
GN NIFS.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022990; PubMed=10555290;
RA Clark M.A.; Moran N.A.; Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
compositions."
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL; AF130814; AAF13805.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 992 MW; F3A73B5047672336 CRC64;

Query Match 26.2%; Score 11; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 6.7e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LYI 7
DB 5 IYL 7

RESULT 14
ID Q9R7T2 PRELIMINARY; PRT; 8 AA.
AC Q9R7T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 1.0 kDa protein (Fragment).
GN Y0R6.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
```

```

RN  SEQUENCE FROM N.A.
RP  STRAIN=R12;
RX  MEDLINE=97061202; PubMed=8905232;
RA  Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA  Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA  Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA  Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA  Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA  Yano M., Horiuchi T.;
RT  "A 718-kb DNA Sequence of Escherichia coli K-12 Genome Corresponding
RT  to the 12,7-28.0 min Region on the Linkage Map.";
RL  DNA Res. 3:137-155(1996).
DR  EMBL; D90705; BAA35310.1; -.
KW  Hypothetical protein.
FT  NON_TER 1
SQ  SEQUENCE 8 AA; 964 MW; DF133B1DD04B476A CRC64;

Query Match 26.2%; Score 11; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 YI 7
DB  3 YI 4

RESULT 15
Q9UHK1 PRELIMINARY; PRT; 8 AA.
AC  Q9UHK1
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DI  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE  01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE  Alpha-1-antitrypsin M-variant (fragment).
GN  ALA.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Ambrose H.J., Chambers S., Miel-Vergani G., Robertson N.H.,
RA  Newton C.R., Ferrie R.M.;
RT  "Molecular characterisation of a new alpha-1-antitrypsin M variant
RT  allele, Mwhitstable: implications for DNA-based diagnosis.";
RL  Diagn. Mol. Pathol. 0:0-0(2000).
DR  EMBL; AF159454; AAF15128.1; -.
FT  NON_TER 1
FT  NON_TER 8
SQ  SEQUENCE 8 AA; 838 MW; 84A732CD331F2CD CRC64;

Query Match 26.2%; Score 11; DB 4; Length 8;
Best Local Similarity 40.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  4 HLYIL 8
DB  3 HKAVL 7

```

Search completed: December 19, 2002, 16:57:39
Job time : 44 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

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. , Run on: December 19, 2002, 16:52:04 ; Search time 34 Seconds
              (without alignments)
              31.353 Million cell updates/sec

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Title: US-09-692-401-6
 Perfect score: 42
 Sequence: 1 RIGHLYII 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 86491

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Minimum DB seq length: 0
Maximum DB seq length: 8
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s

Database :

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2: /SID52/cgcdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SID52/cgcdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SID52/cgcdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SID52/cgcdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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21: /SID52/cgcdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SID52/cgcdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SID52/cgcdata/geneseq/geneseqp-emb1/AA2002.DAT:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	8	22	AAE02084
2	27	64.3	8	22	AAG84724
3	27	64.3	8	22	AAB76030
4	27	64.3	8	23	AAJ00185
5	25	59.5	8	19	AAW79124
6	24	57.1	7	18	AAW17691
7	24	57.1	8	21	AAAB36860
8	24	57.1	8	23	AAU98271
9	23	54.8	6	19	AAW87243
10	23	54.8	6	19	AAW87172
					MAGE-A12 human leu
					MAGE2 HLA-B7 super
					Tumour associated
					MAGE2 derived HLA
					peptide obtained b
					substrate #1 for c
					Angiotensin I conv
					ACE derived peptid
					peptide determined
					peptide determined

11	54.8	8	13	AAR28459	Bombesin antagonist
12	52.4	6	19	AAW57218	Peptide determined
13	52.4	6	19	AAW57429	Peptide determined
14	52.4	7	19	AAW60362	Tumour homing pept
15	52.4	7	20	AAW53688	Human breast cancer
16	52.4	7	21	AAB21779	Human breast tumou
17	52.4	7	22	AAE06357	Human breast tumou
18	52.4	8	7	AAE06971	Polypeptide (CCP-A
19	52.4	8	18	AAV15496	Analogue of urokin
20	52.4	8	18	AAV15386	Analogue of urokin
21	50.0	5	13	AAR28330	Alpha-substituted
22	50.0	5	13	AAR28331	Alpha-substituted
23	50.0	5	13	AAR28332	Alpha-substituted
24	50.0	5	13	AAR28333	Alpha-substituted
25	50.0	5	15	AAAR53122	Cholecystokinin an
26	50.0	5	15	AAAR53123	Cholecystokinin an
27	50.0	5	15	AAAR53124	Cholecystokinin an
28	50.0	5	15	AAAR53125	Cholecystokinin an
29	50.0	6	13	AAAR29389	Endothelin antagon
30	50.0	6	15	AAAR69166	Endothelin C-termi
31	50.0	7	12	AAAR14000	Generic heptapepti
32	50.0	7	12	AAAR15040	Cyclic analogue #5
33	50.0	7	12	AAV08519	Endothelin metal c
34	50.0	7	15	AAAR45750	Bombesin 7-mer ana
35	50.0	7	15	AAAR35759	Bombesin 7-mer ana
36	50.0	7	15	AAAR33760	Bombesin 7-mer ana
37	50.0	7	15	AAAR33761	Bombesin 7-mer ana
38	50.0	7	15	AAAR33762	Bombesin 7-mer ana
39	50.0	7	15	AAAR33763	Bombesin 7-mer ana
40	50.0	7	15	AAAR33764	Bombesin 7-mer ana
41	50.0	7	16	AAW64902	Bombesin receptor
42	50.0	7	19	AAW50964	Bombesin analogue
43	50.0	7	22	AAW77912	C-terminus of a ne
44	50.0	7	22	AAW44415	H11 binding site c
45	50.0	7	22	AAAG64873	Bombesin C-termi

ALIGNMENTS

RESULT 1
AAE02084
ID AAE02084 standard; peptide; 8 AA.

AA
AC
AAE02084:

XX 31-JUL-2007 (first entry)

DE WAGE-A12 human leukocyte antigen-binding peptide #4.

XX Human; cytostatic; immunogen; MAGE-A12; human leukocyte antigen; HLA;
KW CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
KW brain tumour; sarcoma; vaccine; gene therapy

XX
50
Homosexuals
XXXX
BN
W0200129220-02XX
26-APR-2007XX
EE
10-008-3000-300030-17030050

XX	10-008-1000-	0032	016074
XX			

PR 01-FEB-2000; 2000US-0179570.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;

DR WPI; 2001-328498/34.

PT New antigenic peptides derived from MAGE-A12 polypeptides, useful for
PT diagnosis and treatment of cancer, such as bladder, lung, breast,

PT brain, prostate and renal carcinomas
 XX Claim 1; Page 43; 69pp; English.
 CC The patent discloses antigenic peptides derived from MAGE-A12
 CC protein and presented by human leukocyte antigens (HLAs). These
 CC antigenic peptides when presented by an antigen presenting cell
 CC having a HLA class I molecule, effectively induce the activation
 CC and proliferation of CD8+ cytotoxic T lymphocytes. MAGE-A12 is
 CC useful for treating a subject having a disorder characterised by
 CC expression of MAGE-A12. The protein microarray comprising MAGE-A12
 CC is useful for diagnosing a disorder, especially cancer, by determining
 CC the binding of an antibody, T lymphocytes or a HLA molecule isolated
 CC from the subject suspected of having the disorder characterised by the
 CC expression of MAGE-A12. MAGE-A12 is useful for treating cancers
 CC including bladder carcinomas, melanomas, oesophageal, lung, head and
 CC neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas,
 CC prostate and renal carcinomas and to produce antibodies. MAGE-A12
 CC antibodies are useful for diagnosing disorders characterised by
 CC expression of MAGE-A12 immunogenic polypeptide. These MAGE-12 peptides
 CC are used as vaccines. They are also used in gene therapy.
 CC The present sequence is MAGE-A12 HLA class-I-binding peptide. This
 CC antigenic peptide is presented by major histocompatibility complex
 CC (MHC) and is recognised by CTLs.
 XX Sequence 8 AA;
 SQ Query Match 100.0%; Score 42; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIGHLYIL 8
 DB 1 RIGHLYIL 8
 RESULT 2
 AAG84724
 ID AAG84724 standard; Peptide; 8 AA.
 AC AAG84724;
 XX 10-SEP-2001 (first entry)
 DE MAGE2 HLA-B7 supermotif-bearing peptide #7.
 XX Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte;
 KW CTL; MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine;
 KW cancer; cytostatic; immunostimulant.
 XX Homo sapiens.
 OS Synthetic.
 XX WO200142267-A1.
 XX 14-JUN-2001.
 XX 11-DEC-2000; 2000WO-US33545.
 XX 10-DEC-1999; 99US-0458298.
 XX (EPIM-) EPIMMUNE INC.
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 DI Keogh E;
 XX WPI; 2001-375002/39.
 XX An isolated prepared MAGE2/3 epitope (1) for use in pharmaceuticals for
 PT the treatment and prevention of cancer -
 XX Claim 1; Page 155; 171pp; English.

CC The present invention describes MAGE2/3 epitopes (I). Also described
 CC are: (1) a clonal cytotoxic T lymphocyte (CTL) that is cultured in vivo
 CC and binds to a complex of (1); (2) a peptide (II) comprising (1) and a
 CC second epitope and has less than 50 contiguous amino acids; (3) a vaccine
 CC composition comprising (II), a unit dose of a peptide with at least 50
 CC contiguous amino acids with 100% identity to the native peptide sequence
 CC of MAGE2/3, and a pharmaceutical excipient; (4) an isolated nucleic acid
 CC encoding (1); and (5) an isolated nucleic acid encoding (II). (I) has
 CC cytostatic activity, and can be used in vaccines and as an
 CC immunostimulant. A vaccine of (3) is useful for the treatment and
 CC prevention of cancer. (II) is useful for monitoring or evaluating an
 CC immune response by incubating a T-lymphocyte sample from a patient with
 CC (1) that binds to an human leukocyte antigen (HLA) allele present in the
 CC patient and detecting the presence of the T-lymphocyte that binds to the
 CC peptide. The vaccine allows the opportunity to combine epitopes derived
 CC from multiple tumour-associated molecules reducing the likelihood of
 CC tumour escape due to antigen loss. AAG84515 to AAG84909 and AAG9725
 CC represent amino acid sequences used in the exemplification of the
 CC present invention.
 XX Sequence 8 AA;
 SQ Query Match 64.3%; Score 27; DB 22; Length 8;
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 IGHLYI 7
 DB 3 ISHLXI 8
 RESULT 3
 AAB76090
 ID AAB76090 standard; Peptide; 8 AA.
 AC AAB76090;
 XX 10-APR-2001 (first entry)
 DE Tumour associated antigen MAGE2 immunogenic peptide.
 XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
 KW HLA binding peptide; immune response; glycoprotein; cytostatic;
 KW virucide; hepatotropic; antiinflammatory; anti-HIV; vaccine;
 KW human immunodeficiency virus; protozoacide; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; Hpv;
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
 KW condyloma acuminatum.
 XX Homo sapiens.
 OS WO200100225-A1.
 XX 04-JAN-2001.
 XX 28-JUN-2000; 2000WO-US17842.
 XX 29-JUN-1999; 99US-0141422.
 XX (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S;
 DI WPI; 2001-112389/12.
 XX Composition comprising human leukocyte antigen binding peptide which
 PT comprises isolated, prepared epitope useful for treating viral
 PT infections such as acquired immunodeficiency syndrome, and cancer -
 XX Claim 1; Page 47; 58pp; English.

The present invention describes a composition (I) which comprises at least one human leukocyte antigen (HLA) binding peptide comprising an isolated, prepared epitope comprising one of 547 8-11 residue amino acid sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic, virucide, hepatotropic, antinflammatory, anti-HIV (human immunodeficiency virus) and protozoacide activities, which can be used in vaccine production and is an inducer of cytotoxic T-cell response. (I) is useful for inducing a cytotoxic T cell response against a preselcted antigen in a patient expressing a specific major histocompatibility complex (MHC) class I allele, by contacting cytotoxic T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to treat and/or prevent viral infection and cancer such as prostate cancer, hepatitis B, hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma acuminatum.

Sequence 8 AA:

Sequence 8 AA:

Query Match 64.3%; Score 27; DB 22; Length 8;
Best Local Similarity 83.3%; Pred. NO. 7.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels

QY	2	IGHLYI	7
Db	3	ISHLYI	8

RESULT 4

ABJ00185
ID ABJ00185 standard; Peptide; 8 AA.

AC ABJ00185:

30-AUG-2002 (first entry)

DE MAGE2 derived HLA antigen.

Human major histocompatibility complex; HLA; immunogen; cancer; viral infection; vaccine; antigen; anti-HIV; virucide; cytostatic; protozoacide.

Unidentified.

XX
PN
WO200220035-A1.

14-MAR-2002

XX PF 01-SEP-2000: 2000WO-US23913.

XX
PR 01-SEP-2000: 2000W0-11523913XX
PA (EPTM-) EPTMMINE TNC

Sette A. Sidney J. Southwood S.

XX
DR
WPT: 2002-A79A52/51

XX
PT New immunogenic peptide with B7-like supermotif, useful in vaccines
PT against e.g. viral infection and cancer, induces a cytotoxic T cell
PT response

XX
ns
XX

The present invention relates to compositions containing immunogenic peptides, which comprise a B7-like-supermotif. The compositions can be used, as vaccines, to treat or prevent viral diseases (hepatitis B or C, Epstein-Barr, human immune deficiency, Lassa fever or cytomegaloviruses), cancers (e.g. of prostate, kidney or cervix, or lymphoma, where associated with expression of p53, carcino-embryonal antigen or Her2/neu), or malaria. The peptides are also useful as diagnostic agents, e.g. to predict the outcome of a particular therapy and to identify subjects at risk of developing a chronic infection. Nucleic acids

CC encoding the peptides can be used in DNA vaccines. The present sequence
CC is an immunogenic peptide of the invention.

XX	Sequence	8 AA:
SO		

Query Match 64.3%; Score 27; DB 23; Length 8;
Best Local Similarity 83.3%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels

QY	2	IGHLYI	7
Db	3	ISHLYI	8

RESULT 5

AAW79124
ID AAW79124 standard: peptide: 8 AA:

XX
AC AAW79124:XX
DT 18-NOV-1998 (first entry)

peptide obtained by oligomerisation of a minimal motif

xx	Fusion protein; stabilising polypeptide; proteolytic degradation;
xx	resistance; half-life; autoimmune disease; inflammation; vitro drug;
kw	IkappaB regulator protein; inflammatory bowel disease; in vivo imaging;
kw	nitroreductase protein; enzyme therapy; prodrug therapy; protease;
kw	cancer; pathological condition.

XX
OS
Epstein-barr virus.

XX
PN
W09822577-A1

XX
PD
28-MAY-1998XX
PF 17-NOV-1997. 97WQ-TB07508XX
PR 25-JUN-1997. 97IIS-0048945

PR 15-NOV-1996; 96US-0030986.
XX

PA (MASU/) MASUCCI M G.
XX

PI Masucci MG;
XX

DR WPI; 1998-312463/27.
XX

PT New fusion proteins resistant to proteolytic degradation -
PT comprising a core protein with a stabilising polypeptide comprising
PT a peptide sequence containing glycine repeats

XX
PS
Disclosure: page 73: 120pp: English:

Sequences shown in AAW79110 to AAW79125 are obtained by oligomerisation of a selected minimal motif by complementary oligonucleotides. The invention provides a method for increasing the resistance of a core protein to proteolytic degradation that comprises linking or inserting onto or into the core protein a stabilising polypeptide of formula (Gly)₁X(Gly)₁(Gly)₂n where Gly₁, Gly₂, Gly₃ are 1-6 sequential Gly residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, phe, or Thr and n can be anything between 1-66. X, Y and Z need not be identical and n can be anything between 1-66. X, Y and Z need not be identical stabilising polypeptide can be linked onto or inserted into a nucleic acid encoding a core protein. The fusion proteins of the invention are more resistant to degradation by proteases and, thus, have a longer half-life than the untuned core protein. The products can be used for treating autoimmune diseases, cancer and inflammation. In particular, the core protein may be an IkappaB regulator protein for the treatment of inflammatory bowel disease, or a nitroreductase protein which can activate nitro drugs in enzyme/prodrug therapy to treat cancer or other pathological conditions. The fusion proteins can also be used in diagnostic methods such as in vivo imaging.

```

SQ Sequence 8 AA;
Query Match 59.3%; Score 25; DB 19; Length 8;
Best Local Similarity 80.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HLYIL 8
   |||:|
Db 2 HLYLL 6

RESULT 6
AAB17691 standard; peptide; 7 AA.
ID AAB17691
XX
AC AAB17691;
XX
DT 07-JUL-1997 (first entry)
XX
DE Substrate #1 for cathepsin D.
XX
KW Enzyme substrate; MMP-1; protease; tissue abnormality; mesoporphyrin IX;
KW malignancy; mammalian matrix metalloproteinase-1; bacterial collagenase;
KW human interstitial collagenase; cathepsin D; plasmin; fungal infection;
KW human collagenase type IV; mammalian matrix proteinase-2; tissue injury;
KW 72 kd gelatinase; MMP-2; intravascular clotting; bacterial infection;
KW extravascular clotting abnormality; protozoal infection; therapy;
KW parasitic infection.
XX
OS Synthetic.
XX
PN US5618790-A.
XX
PD 08-APR-1997.
XX
PF 05-OCT-1990; 90US-0593867.
XX
PR 16-MAR-1994; 94US-0213897.
XX
PR 05-OCT-1990; 90US-0593867.
XX
PR 10-FEB-1992; 92US-0833183.
XX
PA (TOOH ) UNIV QUEENS KINGSTON.
XX
PI Kennedy JC, Pottier RH, Ringuet M;
XX
DR WPI: 1997-225448/20.
XX
Conjugate system for delivering therapeutic or diagnostic agent to
tissue abnormality site - useful to treat or detect abnormalities
caused by, e.g. malignancy or tissue injuries
Claim 5; Column 18; 10pp; English.
XX
AAB17687-W17698 represent synthetic substrates for proteases known to be
active in and/or immediately adjacent to certain specified cell or
tissue abnormalities. This sequence is a substrate for cathepsin D.
These sequences can be used in the conjugate system of the invention.
The conjugate system is for delivering a therapeutic or diagnostic agent
to a tissue abnormality site (TAS) in a patient. The system comprises a
lipophilic or amphiphilic agent, covalently linked to a protease
sensitive polypeptide (such as this sequence) having an amino acid
sequence readily cleavable by a protease active at the TAS, but not at a
normal tissue site and a solubility modifier conjugated to the protease
sensitive polypeptide. Peptides sensitive to cleavage by bacterial
collagenase, mammalian matrix metalloproteinase-1, plasmin, human
proteinase-2, or MMP-2), or mesoporphyrin IX, can also be used in the
system. The system can be used to treat or detect tissue abnormalities
caused by malignancy, tissue injuries, intravascular or extravascular
clotting abnormalities or bacterial, fungal, protozoal or parasitic
infections.
XX
Sequence 7 AA;

```

```

Query Match 57.1%; Score 24; DB 18; Length 7;
Best Local Similarity 50.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GHLYIL 8
   ||:|
Db 2 GHFFVL 7

RESULT 7
AAB26860 standard; peptide; 8 AA.
ID AAB26860
XX
AC AAB26860;
XX
DT 30-JAN-2001 (first entry)
XX
DE Angiotensin I converting enzyme (ACE) inhibitory peptide 3.
XX
KW Angiotensin I converting enzyme; ACE; ACE inhibitor; hypotensive agent.
XX
OS Synthetic.
XX
PN JP200029996-A.
XX
PD 22-AUG-2000.
XX
PF 08-FEB-1999; 99JP-0030663.
XX
PR 08-FEB-1999; 99JP-0030663.
XX
PA (TOHA-) TOYO HAKKO KK.
XX
DR WPI: 2000-614869/59.
XX
PT Angiotensin I converting enzyme inhibitory octapeptides useful as
hypotensive agents, and a process for their preparation -
XX
PS Claim 5; Page 2; 11pp; Japanese.
XX
This invention relates to the preparation of angiotensin I converting
enzyme (ACE) inhibitors by a microbiological process. The inhibitors are
useful as hypotensive agents, and heat resistant ACE inhibitors are used
in food processing. The invention includes examples of ACE I inhibitory
peptides, represented by sequences AAB26858-B26868.
XX
Sequence 8 AA;
Query Match 57.1%; Score 24; DB 21; Length 8;
Best Local Similarity 50.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IGHLYI 7
   ||:|
Db 1 ISHIYV 6

RESULT 8
AAU98271 standard; peptide; 8 AA.
ID AAU98271
XX
AC AAU98271;
XX
DT 15-AUG-2002 (first entry)
XX
DE ACE derived peptide P2.
XX
KW Peptide production; fusion peptide; histidine tag; enterokinase; ACE.
XX
OS Oryza sativa.
XX
OS Glycine max.
XX

```

```
PN JP2002119284-A.
PD
PD 23-APR-2002.
PF
PF 13-OCT-2000; 2000JP-0313609.
PR
PR 13-OCT-2000; 2000JP-0313609.
XX
XX (TOHA-) TOYO HAKKO KK.
PA
PA WPI; 2002-475328/51.
DR
XX A process for preparation of short length peptides by culture of a
PT transformant with an expression vector, followed by cleavage with an
PT enzyme recognising the selective enzyme cleavage site -
PT
PS Example 1; Page 9; 12pp; Japanese.
XX
XX The invention relates to a process for preparation of short length
XX peptides by culture of a transformant with an expression vector,
XX prepared by insertion of a gene encoding the fused peptide with the
XX short peptide and the selective enzyme cleavage site, containing 2 or
XX more genes encoding for a fused peptide with a short length peptide,
XX particularly containing a histidine tag, and a selective enzyme
XX cleavage site, particularly the site with cleaved enterokinase,
XX followed by cleavage with the enzyme recognising the selective enzyme
XX cleavage site. The method involves selective cleavage of long chain
XX peptides to give the aimed short length peptide. The present
XX sequence is a peptide derived from the ACE protein (not defined)
XX suitable for production using the method of the invention.
XX
XX Sequence 8 AA;
SQ
Query Match 57.1%; Score 24; DB 23; Length 8;
Best Local Similarity 50.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 IGHLIY 7
DB 1 ISHIIV 6
RESULT 9
AAW87243
ID AAW87243 standard; peptide; 6 AA.
AC AAW87243;
XX
XX 09-FEB-1999 (first entry)
DT
DE Peptide determined by the method of the invention.
XX
XX Amino acid determination; molecular mass; fragmentation spectrum;
KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.
XX
XX Synthetic.
OS
XX GB2325465-A.
PN
PD 25-NOV-1998.
XX
XX 22-MAY-1998; 98GB-0011196.
PF
XX 22-MAY-1997; 97GB-0010582.
PR
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
PA Parekh RB, Prime SB, Townsend RR, Wedd NS;
PI
PI WPI; 1998-571195/49.
DR
XX
XX Peptide sequence determination used in e.g. DNA cloning - by
PT comparing mass spectra of the unknown peptide with a library of
PT
```

```
PT linear chain known peptide sequences
XX
XX Example 1; Page 20; 40pp; English.
XX
XX The invention relates to a method for determination of the amino acid
XX sequence of an unknown peptide. The method comprises (a) determining
XX the molecular mass and an experimental fragmentation spectrum for the
XX peptide; (b) comparing the experimental fragmentation spectrum of the
XX unknown peptide with a theoretical fragmentation spectra calculated for
XX a peptide library composed of all possible linear sequences of amino
XX acids having a total mass that corresponds to the molecular mass of the
XX unknown peptide; and (c) identifying a peptide in the library with a
XX theoretical fragmentation spectrum that most closely matches the
XX fragmentation spectrum of the unknown peptide. The method is useful in
XX DNA cloning, anti-body production, identification of recombinant
XX products, and the study of post-translational modifications. It allows
XX the sequence of unknown peptides or proteins with no sub-sequences
XX identity, to be characterised using mass spectrometry. Sequences
XX AAW87101 to AAW87364 represent a library of linear peptides constructed
XX to exemplify the method. The isoleucine residue in these peptides can be
XX replaced by leucine to construct another 264 linear peptides to be
XX included in the library.
XX
XX Sequence 6 AA;
SQ
Query Match 54.8%; Score 23; DB 19; Length 6;
Best Local Similarity 75.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 GHLY 6
DB 2 GHIV 5
RESULT 10
AAW87172
ID AAW87172 standard; peptide; 6 AA.
AC AAW87172;
XX
XX 09-FEB-1999 (first entry)
DT
DE Peptide determined by the method of the invention.
XX
XX Amino acid determination; molecular mass; fragmentation spectrum;
KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.
XX
XX Synthetic.
OS
XX GB2325465-A.
PN
PD 25-NOV-1998.
XX
XX 22-MAY-1998; 98GB-0011196.
PF
XX 22-MAY-1997; 97GB-0010582.
PR
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA
PA Parekh RB, Prime SB, Townsend RR, Wedd NS;
PI
PI WPI; 1998-571195/49.
DR
XX
XX Peptide sequence determination used in e.g. DNA cloning - by
PT comparing mass spectra of the unknown peptide with a library of
PT linear chain known peptide sequences
XX
XX Example 1; Page 20; 40pp; English.
XX
XX The invention relates to a method for determination of the amino acid
XX sequence of an unknown peptide. The method comprises (a) determining
XX the molecular mass and an experimental fragmentation spectrum for the
XX peptide; (b) comparing the experimental fragmentation spectrum of the
XX unknown peptide with a theoretical fragmentation spectra calculated for
XX a peptide library composed of all possible linear sequences of amino
XX acids having a total mass that corresponds to the molecular mass of the
XX unknown peptide; and (c) identifying a peptide in the library with a
XX theoretical fragmentation spectrum that most closely matches the
XX fragmentation spectrum of the unknown peptide. The method is useful in
XX DNA cloning, anti-body production, identification of recombinant
XX products, and the study of post-translational modifications. It allows
XX the sequence of unknown peptides or proteins with no sub-sequences
XX identity, to be characterised using mass spectrometry. Sequences
XX AAW87101 to AAW87364 represent a library of linear peptides constructed
XX to exemplify the method. The isoleucine residue in these peptides can be
XX replaced by leucine to construct another 264 linear peptides to be
XX included in the library.
XX
XX Sequence 6 AA;
SQ
```

CC unknown peptide with a theoretical fragmentation spectra calculated for
 CC a peptide library composed of all possible linear sequences of amino
 CC acids having a total mass that corresponds to the molecular mass of the
 CC unknown peptide; and (c) identifying a peptide in the library with a
 CC theoretical fragmentation spectrum that most closely matches the
 CC fragmentation spectrum of the unknown peptide. The method is useful in
 CC DNA cloning, anti-body production, identification of recombinant
 CC products, and the study of post-translational modifications. It allows
 CC the sequence of unknown peptides or proteins with no sub-sequence
 CC identity to be characterised using mass spectrometry. Sequences
 CC AAW87101 to AAW87364 represent a library of linear peptides constructed
 CC to exemplify the method. The isoleucine residue in these peptides can be
 CC replaced by leucine to construct another 264 linear peptides to be
 CC included in the library.

XX Sequence 6 AA;
 SQ

Query Match 54.8%; Score 23; DB 19; Length 6;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GHLY 6
 DB 1 GHLY 4

RESULT 11
 AAR28459
 ID AAR28459 standard; Protein; 8 AA.
 AC AAR28459;
 DT 09-DEC-1992 (first entry)
 DE Bombesin antagonist (27).
 XX Bombesin; GRP; gastrin releasing peptide.
 KW Bombesin; GRP; gastrin releasing peptide.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1 /note= "Mpp-Gln; Mpp= 3-(4-methoxyphenyl)
 FT Modified-site 7 /label= psi
 FT /note= "residues 7-8 are linked via a pseudo
 FT Modified-site 8 /label= psi
 FT /note= "Trp(For), For= formyl; residues 7-8 are
 FT linked via a pseudo peptide bond"

XX WO9209626-A.
 XX
 XX 11-JUN-1992.
 XX
 XX 15-NOV-1991; 91WO-US08534.
 XX
 XX 29-NOV-1990; 90US-0619747.
 XX
 XX (TULA) TULANE EDUCATIONAL FUND.
 XX
 XX Cai RZ, Schally AV;
 XX
 XX WPT; 1992-217019/26.
 XX
 XX New nona-peptide bombesin antagonists - used for treating
 PT hypergastrinaemic states, such as pernicious anaemia and
 PT Zollinger-Ellison syndrome and also used against lung and gastric
 PT cancer, etc.
 XX
 XX Disclosure; Page 8; 50pp; English.

XX The C-terminal is amidated. The peptide is an example of a highly
 CC generic formula for bombesin antagonists which are [psi18-9 pseudo]
 CC nonapeptides contg. D- or L-tryptophan or tryptophan analog
 CC 2,3,4,9-tetrahydro-1H-pyrido[3,4-b]-indol-3-carboxylic acid (Tpi)
 CC at the N- and/or C-terminal.
 CC The peptide is a bombesin/GRP (gastrin releasing peptide) antagonist
 CC and is useful for treatment of states of hypergastrinemia, e.g.
 CC pernicious anaemia, chronic atrophic gastritis, Zollinger-Ellison
 CC syndrome and vitiligo associated with diffuse hyperplasia of
 CC gastric enterochromaffin-like cells, and with an increased risk of
 CC developing multifocal gastric carcinoma tumours. The peptide can
 CC also be used to treat lung, colon and gastric cancers. Dosage is
 CC 1- 1000 microg/kg parenterally.

XX Sequence 8 AA;
 SQ

Query Match 54.8%; Score 23; DB 13; Length 8;
 Best Local Similarity 60.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGHLY 6
 DB 4 VGHLY 8

RESULT 12
 AAW87218
 ID AAW87218 standard; peptide; 6 AA.
 AC AAW87218;
 DT 09-FEB-1999 (first entry)
 DE Peptide determined by the method of the invention.
 XX Amino acid determination; molecular mass; fragmentation spectrum;
 KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.
 OS Synthetic.

XX GB2325465-A.
 XX 25-NOV-1998.
 XX 22-MAY-1998; 98GB-0011196.
 XX 22-MAY-1997; 97GB-0010582.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Parekh RB, Prime SB, Townsend RR, Wedd NS;
 XX WPI; 1998-571195/49.
 XX
 XX Peptide sequence determination used in e.g. DNA cloning - by
 PT comparing mass spectra of the unknown peptide with a library of
 PT linear chain known peptide sequences
 XX
 XX Example 1; Page 19; 40pp; English.

XX The invention relates to a method for determination of the amino acid
 CC sequence of an unknown peptide. The method comprises (a) determining
 CC the molecular mass and an experimental fragmentation spectrum of the
 CC peptide; (b) comparing the experimental fragmentation spectrum of the
 CC unknown peptide with a theoretical fragmentation spectra calculated for
 CC a peptide library composed of all possible linear sequences of amino
 CC acids having a total mass that corresponds to the molecular mass of the
 CC unknown peptide; and (c) identifying a peptide in the library with a
 CC theoretical fragmentation spectrum that most closely matches the
 CC fragmentation spectrum of the unknown peptide. The method is useful in
 CC DNA cloning, anti-body production, identification of recombinant
 CC products, and the study of post-translational modifications. It allows

CC the sequence of unknown peptides or proteins with no sub-sequence
 CC identity, to be characterised using mass spectrometry. Sequences
 CC AAW87101 to AAW87364 represent a library of linear peptides constructed
 CC to exemplify the method. The isoleucine residue in these peptides can be
 CC replaced by leucine to construct another 264 linear peptides to be
 CC included in the library.

XX SQ Sequence 6 AA;

Query Match 52.4%; Score 22; DB 19; Length 6;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 GHLYI 7
 DB 1 GHEYI 5

RESULT 13
 AAW87229
 ID AAW87229 standard; peptide; 6 AA.

XX AC AAW87229;

XX DT 09-FEB-1999 (first entry)

XX DE Peptide determined by the method of the invention.

XX KW Amino acid determination; molecular mass; fragmentation spectrum;
 KW DNA cloning; anti-body; recombinant; modification; mass spectrometry.

XX OS Synthetic.

XX PN GB2325465-A.

XX PD 25-NOV-1998.

XX PF 22-MAY-1998; 98GB-0011196.

XX PR 22-MAY-1997; 97GB-0010582.

XX PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.

XX PI Parekh RB, Prime SB, Townsend RR, Wedd NS;

XX DR WPI; 1998-571195/49.

XX PT Peptide sequence determination used in e.g. DNA cloning - by
 PT comparing mass spectra of the unknown peptide with a library of
 PT linear chain known peptide sequences

XX PS Example 1; Page 20; 40pp; English.

XX CC The invention relates to a method for determination of the amino acid
 CC sequence of an unknown peptide. The method comprises (a) determining
 CC the molecular mass and an experimental fragmentation spectrum for the
 CC peptide; (b) comparing the experimental fragmentation spectrum of the
 CC unknown peptide with a theoretical fragmentation spectra calculated for
 CC a peptide library composed of all possible linear sequences of amino
 CC acids having a total mass that corresponds to the molecular mass of the
 CC unknown peptide; and (c) identifying a peptide in the library with a
 CC theoretical fragmentation spectrum that most closely matches the
 CC fragmentation spectrum of the unknown peptide. The method is useful in
 CC DNA cloning, anti-body production, identification of recombinant
 CC products, and the study of post-translational modifications. It allows
 CC the sequence of unknown peptides or proteins with no sub-sequence
 CC identity, to be characterised using mass spectrometry. Sequences
 CC AAW87101 to AAW87364 represent a library of linear peptides constructed
 CC to exemplify the method. The isoleucine residue in these peptides can be
 CC replaced by leucine to construct another 264 linear peptides to be
 CC included in the library.

XX SQ Sequence 6 AA;

Query Match 52.4%; Score 22; DB 19; Length 6;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 IGHLY 6
 DB 1 IGHEY 5

RESULT 14
 AAW60362
 ID AAW60362 standard; peptide; 7 AA.

XX AC AAW60362;

XX DT 24-AUG-1998 (first entry)

XX DE Tumour homing peptide of the invention.

XX KW Tumour homing peptide; in vivo panning;

XX KW alpha-v-containing integrin binding motif; tumour.

XX OS Synthetic.

XX PN WO9810795-A2.

XX PD 19-MAR-1998.

XX PF 10-SEP-1997; 97WO-US16086.

XX PR 10-SEP-1996; 96US-0710067.

XX PA (BURN-) BURNHAM INST.

XX PI Pasqualini R, Ruoslahti E;

XX DR WPI; 1998-207151/18.

XX PT Tumour homing molecules and their conjugates - useful for, e.g.
 PT directing linked moiety to tumour containing angiogenic vasculature

XX PS Example 3; Page 74; 105pp; English.

XX CC AAW60303-89 represent peptides recovered from human breast cancer.
 CC The peptides are tumour homing peptides, and are identified by in
 CC vivo panning. The in vivo panning comprises administering a library
 CC of diverse peptides to a subject having a tumour, collecting a sample of
 CC the tumour, identifying a peptide that homes to the tumour, collecting a
 CC sample of normal tissue corresponding to the tumour, and determining
 CC that the peptide that homes to the tumour is not present in the normal
 CC tissue. The tumour homing peptides can be linked to a moiety (e.g.
 CC doxorubicin), and used to direct the moiety to a tumour.

XX SQ Sequence 7 AA;

Query Match 52.4%; Score 22; DB 19; Length 7;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RIGHL 5
 DB 3 RTGHL 7

RESULT 15
 AAW93688
 ID AAW93688 standard; peptide; 7 AA.

XX AC AAW93688;

XX DT 28-JUN-1999 (first entry)

DE Human breast cancer derived tumour homing peptide 60.
 XX Tumour homing peptide; tumour; diagnosis; endothelial cell; breast;
 KW angiogenic vasculature; anti-tumour; anti-inflammatory; anti-angiogenic;
 KW anti-arthritis; NGR receptor; inhibitor; angiogenesis; anticancer drug;
 KW prognosis; inflammation; regeneration; wounded tissue; targeting;
 KW macular degeneration; diabetic retinopathy; rheumatoid arthritis;
 KW occlusive thrombus; human.
 XX
 OS Homo sapiens.
 XX
 PN WO9913329-A1.
 XX
 PD 18-MAR-1999.
 XX
 PF 08-SEP-1998; 98WO-US18895.
 XX
 PR 25-AUG-1998; 98US-0139802.
 PR 10-SEP-1997; 97US-0926914.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 PI Pasqualini R, Ruoslahti E;
 DR WPI; 1999-215158/18.
 XX
 PT Identifying molecules that home to angiogenic vasculature used as
 PT targets for anticancer agents
 XX
 PS Example II; Page 104; 180pp; English.
 XX
 CC This invention describes novel peptides which home to angiogenic
 CC vasculature, specifically of a tumour and which have anti-tumour,
 CC anti-inflammatory, anti-angiogenic and anti-arthritis activity. Such
 CC molecules are identified by treating a purified NGR receptor with a test
 CC compound and identifying compounds that bind specifically to the NGR
 CC receptor. The peptides of the invention are inhibitors of angiogenesis
 CC and can be used to produce conjugates for delivering agents to
 CC angiogenic vasculature, particularly anticancer drugs or an imaging
 CC agent, for diagnosis or prognosis. These conjugates may be directed to
 CC non-tumour angiogenic vasculature, e.g. that present in inflammatory,
 CC regenerating or wounded tissue, e.g. for treatment of macular
 CC degeneration, diabetic retinopathy or rheumatoid arthritis. The peptides
 CC provide specific targeting to tumours, especially their supporting
 CC vasculature, since the NGR receptor is exposed to the circulation only in
 CC angiogenic vasculature. Precise targeting should reduce the systemic
 CC toxicity of anticancer drugs in the conjugates. Complete killing of all
 CC target cells may not be essential since partial denudation of endothelium
 CC may result in an occlusive thrombus, and endothelial cells are unlikely
 CC to become resistant to anticancer agents nor to lose the targeting
 CC receptor. AAW93622-W93809 and AAW93843-44 are examples of tumour homing
 CC peptides used in the invention.
 XX
 SQ Sequence 7 AA;
 Query Match 52.4%; Score 22; DB 20; Length 7;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 RIGHL 5
 Db 3 RTGHL 7

Search completed: December 19, 2002, 16:56:33
 Job time : 40 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:57:45 : Search time 11 Seconds
(without alignments)
12.192 Million cell updates/sec

Title: US-09-692-401-6

Perfect score: 42

Sequence: 1 RIGHLYIL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 106657 seqs, 16763532 residues

Total number of hits satisfying chosen parameters: 13268

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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2: /cgn2.6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2.6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
4: /cgn2.6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
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9: /cgn2.6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
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11: /cgn2.6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2.6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2.6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2.6/ptodata/2/pubpaa/US60_PUBCOMB pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	27	64.3	8	9	US-09-017-743C-100
2	22	52.4	7	10	US-09-765-086-79
3	21	50.0	7	10	US-09-730-801-1
4	21	50.0	8	9	US-09-766-347-1
5	21	50.0	8	10	US-09-756-875-16
6	21	50.0	8	10	US-09-756-875-17
7	19	45.2	6	9	US-09-813-718-42
8	19	45.2	7	8	US-08-812-393A-51
9	19	45.2	7	9	US-10-080-100-86
10	19	45.2	7	10	US-09-824-286-14
11	19	45.2	7	10	US-09-731-242A-24
12	19	45.2	7	10	US-09-901-187B-10
13	19	45.2	8	9	US-09-766-889A-10
14	19	45.2	8	10	US-09-071-838-45
15	18	42.9	7	9	US-10-080-100-83
16	18	42.9	7	10	US-09-765-086-139
17	18	42.9	7	10	US-09-989-789-172
18	18	42.9	7	10	US-09-989-789-173
19	18	42.9	7	10	US-09-989-789-235

20	18	42.9	7	10	US-09-989-789-257
21	18	42.9	7	10	US-09-989-789-281
22	18	42.9	7	10	US-09-989-789-282
23	18	42.9	7	10	US-09-989-789-283
24	18	42.9	7	10	US-09-989-789-284
25	18	42.9	7	10	US-09-989-789-287
26	18	42.9	7	10	US-09-989-789-290
27	18	42.9	7	10	US-09-989-789-313
28	18	42.9	7	10	US-09-989-789-318
29	18	42.9	7	10	US-09-989-789-330
30	18	42.9	7	10	US-09-989-789-393
31	18	42.9	7	10	US-09-989-789-407
32	18	42.9	7	10	US-09-989-789-413
33	18	42.9	7	10	US-09-989-789-432
34	18	42.9	7	10	US-09-989-789-738
35	18	42.9	7	10	US-09-989-789-809
36	18	42.9	7	10	US-09-989-789-812
37	18	42.9	7	10	US-09-989-789-825
38	18	42.9	7	10	US-09-989-789-837
39	18	42.9	7	10	US-09-989-789-838
40	18	42.9	7	10	US-09-989-789-841
41	18	42.9	7	10	US-09-989-789-935
42	18	42.9	7	10	US-09-989-789-936
43	18	42.9	7	10	US-09-989-789-937
44	18	42.9	7	10	US-09-989-789-944
45	18	42.9	7	10	US-09-989-789-957

ALIGNMENTS

RESULT 1
US-09-017-743C-100
: Sequence 100, Application US/09017743C
: Patent No. US20020177694A1
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
: Sidney, John
: TITLE OF INVENTION: HLA Binding Peptides and Their Uses
: NUMBER OF SEQUENCES: 146
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/017,743C
: FILING DATE: 03-Feb-1998
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/590,298
: FILING DATE: 23-JAN-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Parent, Annette S.
: REGISTRATION NUMBER: 42,058
: REFERENCE/DOCKET NUMBER: 018623-008050US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 415-576-0300
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 100:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid

Sequence 257, App
Sequence 281, App
Sequence 282, App
Sequence 283, App
Sequence 284, App
Sequence 287, App
Sequence 297, App
Sequence 313, App
Sequence 318, App
Sequence 330, App
Sequence 393, App
Sequence 407, App
Sequence 413, App
Sequence 432, App
Sequence 438, App
Sequence 738, App
Sequence 809, App
Sequence 812, App
Sequence 825, App
Sequence 837, App
Sequence 838, App
Sequence 841, App
Sequence 935, App
Sequence 936, App
Sequence 937, App
Sequence 944, App
Sequence 957, App

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-017-743C-100

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Query Match      64.3%; Score 27; DB 9; Length 8;
Best Local Similarity 83.3%; Pred. No. 8.9e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy  2  IGHLV 7
    1  ||||
Db  3  ISHLVI 8

```

RESULT 2

```

US-09-765-086-79
; Sequence 79, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Wadli, Arap
; APPLICANT: Bredesen, Dale E.
; APPLICANT: Ellerby, H. Michael
; TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
; FILE REFERENCE: P-LJ 3844
; CURRENT APPLICATION NUMBER: US 09/765,086
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 09/489,582
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 235
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 79
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-765-086-79

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```

Query Match      52.4%; Score 22; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 8.9e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy  1  RIGHL 5
    1  |||
Db  3  RTGHL 7

```

RESULT 3

```

US-09-730-801-1
; Sequence 1, Application US/09730801
; Patent No. US20020103132A1
; GENERAL INFORMATION:
; APPLICANT: Kusk, Kenneth A.
; TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal
; IMMUNITY
; FILE REFERENCE: 44137-5001-01-US
; CURRENT APPLICATION NUMBER: US/09/730,801
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US/09/067,032
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 08/842,877
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: 60/029,689
; PRIOR FILING DATE: 1996-10-31
; PRIOR APPLICATION NUMBER: US 60/015,835
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

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```

; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-801-1

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```

Query Match      50.0%; Score 21; DB 10; Length 7;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy  2  IGHL 5
    1  |||
Db  3  VGHL 6

```

RESULT 4

```

US-09-766-347-1
; Sequence 1, Application US/09766347
; Patent No. US20020169107A1
; GENERAL INFORMATION:
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Cantrell, Gary
; APPLICANT: Achillefu, Samuel
; APPLICANT: Bugaj, Joseph
; APPLICANT: Dorshow, Richard
; APPLICANT: Mallinckrodt Inc.
; TITLE OF INVENTION: NOVEL AROMATIC AZIDES FOR TYPE I PHOTOTHERAPY
; FILE REFERENCE: MRD-60
; CURRENT APPLICATION NUMBER: US/09/766,347
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent In Version 3.1
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)...(8)
; OTHER INFORMATION: Bombesin analog
US-09-766-347-1

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```

Query Match      50.0%; Score 21; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy  2  IGHL 5
    1  |||
Db  4  VGHL 7

```

RESULT 5

```

US-09-756-875-16
; Sequence 16, Application US/09756875
; Patent No. US20020150990A1
; GENERAL INFORMATION:
; APPLICANT: PIKE, IAN
; TITLE OF INVENTION: HEPATITIS C VIRUS PEPTIDES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 701-E Columbia Square
; STREET: 555 13th Street, N. W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: U. S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,875
; FILING DATE:

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; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-812-393A-51

Query Match          45.2%; Score 19; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.9e+04; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 4 HLX 6
DB 1 HLX 3

RESULT 9
US-10-080-100-86
; Sequence 86, Application US/10080100
; Patent No. US20020165356A1
; GENERAL INFORMATION:
; APPLICANT: Barbas, Carlos
; TITLE OF INVENTION: Zinc Finger Binding Domains for
; FILE REFERENCE: TSRI 760.0
; CURRENT APPLICATION NUMBER: US/10/080,100
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US/09/791,106
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-080-100-86

Query Match          45.2%; Score 19; DB 9; Length 7;
Best Local Similarity 60.0%; Pred. No. 8.9e+04; Indels 1;
Matches 3; Conservative 1; Mismatches 1; Gaps 0;

QY 3 GHLXI 7
DB 3 GHLRV 7

RESULT 10
US-09-824-286-14
; Sequence 14, Application US/09824286
; Patent No. US20020028202A1
; GENERAL INFORMATION:
; APPLICANT: Burkly, Linda C
; Benjamin, Christopher D
; Hession, Catherine A
; Whitty, Adrian
; TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Biogen, Inc.
; STREET: 14 Cambridge Center
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02142
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,286
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017,466
; FILING DATE: 10-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ksolan, Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: A006 PCT CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 679-2838
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-824-286-14

Query Match          45.2%; Score 19; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.9e+04; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 4 HLX 6
DB 4 HLX 6

RESULT 11
US-09-731-242A-24
; Sequence 24, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,179
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 7
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: ( ) ( )
; OTHER INFORMATION: CDR3alpha sequence
US-09-731-242A-24

Query Match          45.2%; Score 19; DB 10; Length 7;
Best Local Similarity 66.7%; Pred. No. 8.9e+04; Indels 2;
Matches 4; Conservative 0; Mismatches 2; Gaps 0;

QY 3 GHLXIL 8
DB 2 GHLPL 7

```

RESULT 12

US-09-901-187B-10
; Sequence 10, Application US/09901187B
; Patent No. US20020131464A1
; GENERAL INFORMATION:
; APPLICANT: Paraceta Pharmaceuticals, Inc.
; APPLICANT: Molozin, Benjamin
; APPLICANT: Ostretova-Golts, Natalie
; APPLICANT: Lebowitz, Michael S.
; TITLE OF INVENTION: Methods for Preventing Neural Tissue Damage and for the Treatment
; FILE REFERENCE: PAM01/002US
; CURRENT APPLICATION NUMBER: US/09/901,187B
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,319
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/279,199
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-187B-10

Query Match 45.2%; Score 19; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HLX 6
DB 1 HLX 3

RESULT 13

US-03-766-889A-10
; Sequence 10, Application US/09766889A
; Patent No. US20020164634A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schults, Erwin
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-10

Query Match 45.2%; Score 19; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GHLY 6
DB 5 GHSY 8

RESULT 14

US-09-071-838-45

; Sequence 45, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-0861000S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-45

Query Match 45.2%; Score 19; DB 10; Length 8;
Best Local Similarity 57.1%; Pred. No. 8.9e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIGHLY 7
DB 1 KIIVLYI 7

RESULT 15

US-10-080-100-83
; Sequence 83, Application US/10080100
; Patent No. US20020165356A1
; GENERAL INFORMATION:
; APPLICANT: Barbados, Carlos
; APPLICANT: Dreier, Birgit
; TITLE OF INVENTION: Zinc Finger Binding Domains for
; FILE REFERENCE: TSRI 760.0
; CURRENT APPLICATION NUMBER: US/10/080,100
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US/09/791,106
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: synthesized
US-10-080-100-83
Query Match      42.9%  Score 18; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 GHL 5
Db      111
Db      3 GHL 5
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Search completed: December 19, 2002, 17:01:39
Job time : 19 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 19, 2002, 16:55:55 ; Search time 14 Seconds
(without alignments)
16.813 Million cell updates/sec

Title: US-09-692-401-6

Perfect score: 42

Sequence: 1 RIGHLYIL 8

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Searched: 262574 seqs, 2942292 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	25	59.5	8	2	US-08-529-190B-45
2	24	57.1	7	1	US-08-213-897A-5
3	22	52.4	7	4	US-09-139-802-79
4	21	50.0	7	1	US-08-168-390-3
5	21	50.0	7	3	US-08-974-775-48
6	21	50.0	7	4	US-08-530-342A-15
7	21	50.0	7	4	US-09-473-355-1
8	21	50.0	7	4	US-09-067-032-1
9	21	50.0	7	6	5217955-30
10	21	50.0	7	6	5460801-3
11	21	50.0	8	1	US-08-168-390-11
12	21	50.0	8	1	US-08-168-390-13
13	21	50.0	8	1	US-08-387-634-3
14	21	50.0	8	2	US-08-337-127-9
15	21	50.0	8	4	US-08-444-818-258
16	21	50.0	8	4	US-08-444-818-259
17	21	50.0	8	4	US-09-260-846-9
18	21	50.0	8	6	5217955-27
19	21	50.0	8	6	5217955-28
20	21	50.0	8	6	5217955-32
21	21	50.0	8	6	5217955-34
22	20	47.6	8	2	US-08-529-190B-64
23	19	45.2	6	1	US-08-014-979-80
24	19	45.2	6	2	US-08-174-109A-59
25	19	45.2	6	2	US-08-687-706-39
26	19	45.2	6	2	US-08-482-228-126
27	19	45.2	6	3	US-08-482-528-126

28	19	45.2	7	4	US-09-189-129-14	Sequence 14, Appl
29	19	45.2	7	4	US-09-020-065A-2	Sequence 2, Appl
30	19	45.2	8	1	US-07-938-334C-22	Sequence 22, Appl
31	19	45.2	8	1	US-08-073-103A-14	Sequence 14, Appl
32	19	45.2	8	1	US-08-159-340A-22	Sequence 22, Appl
33	19	45.2	8	1	US-08-457-804-4	Sequence 4, Appl
34	19	45.2	8	1	US-08-457-804-11	Sequence 11, Appl
35	19	45.2	8	1	US-08-443-341-14	Sequence 14, Appl
36	19	45.2	8	3	US-08-354-679C-14	Sequence 14, Appl
37	19	45.2	8	4	US-08-393-273E-14	Sequence 14, Appl
38	19	45.2	8	4	US-09-177-249-45	Sequence 45, Appl
39	19	45.2	8	4	US-08-160-604-46	Sequence 46, Appl
40	19	45.2	8	4	US-08-160-604-47	Sequence 47, Appl
41	19	45.2	8	4	US-08-443-580F-14	Sequence 14, Appl
42	18.5	44.0	8	1	US-08-457-804-12	Sequence 12, Appl
43	18	42.9	4	2	US-08-685-589A-51	Sequence 51, Appl
44	18	42.9	5	1	US-08-014-979-51	Sequence 51, Appl
45	18	42.9	5	2	US-08-966-388-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-529-190B-45
Sequence 45, Application US/08529190B
Patent No. 5835991
GENERAL INFORMATION:
APPLICANT: Masucci, Maria G
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
TITLE OF INVENTION: CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,190B
FILING DATE: 15-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE9501324-9
FILING DATE: 10-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/522,595
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen A
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3255/53015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111

INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-529-190B-45

Query Match 59.5%; Score 25; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

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QY 4 HLXIL 8
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Db 2 HLXLL 6

RESULT 2
US-08-213-897A-5
; Sequence 5, Application US/08213897A
; Patent No. 5618790
; GENERAL INFORMATION:
; APPLICANT: Protease Mediated Drug Delivery System
; TITLE OF INVENTION: 18
; NUMBER OF SEQUENCES: 18
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION NUMBER: US/08/213,897A
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/593,867
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/833,183
; FILING DATE: 10-FEB-1992
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-213-897A-5

Query Match 57.1%; Score 24; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GHLXIL 8
    |||:|
Db 2 GHEFVL 7

RESULT 3
US-09-139-802-79
; Sequence 79, Application US/09139802
; Patent No. 6180084
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
; TITLE OF INVENTION: Same
; FILE REFERENCE: P-LJ 3203
; CURRENT APPLICATION NUMBER: US/09/139,802
; CURRENT FILING DATE: 1998-08-25
; EARLIER APPLICATION NUMBER: 08/926,914
; EARLIER FILING DATE: 1997-09-10
; EARLIER APPLICATION NUMBER: 08/710,067
; EARLIER FILING DATE: 1996-09-10
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 79
; LENGTH: 7
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-139-802-79

Query Match 52.4%; Score 22; DB 4; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIGHL 5
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Db 3 RTGHL 7

RESULT 4
US-08-168-390-3
; Sequence 3, Application US/08168390
; Patent No. 5620955
; GENERAL INFORMATION:
; APPLICANT: Knight, Martha
; APPLICANT: Takahashi, Kazuyuki
; APPLICANT: Chandrasekhar, Bhaskar
; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/168,390
; FILING DATE: Herewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0871.0040001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; TELEX: 248636 SSK
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "The amino-terminal residue
; OTHER INFORMATION: comprises one of several chemical end caps."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "The carboxy-terminal
; OTHER INFORMATION: residue comprises an ethyl ester."
US-08-168-390-3

Query Match 50.0%; Score 21; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGHL 5
    |||
Db 4 VGHL 7

RESULT 5
US-08-974-775-48
; Sequence 48, Application US/08974775
; Patent No. 6096706
```



```

; GENERAL INFORMATION:
; APPLICANT: Toback, F. Gary
; APPLICANT: Walsh-Reitz, Margaret
; TITLE OF INVENTION: GROWTH-PROMOTING PROTEINS AND PEPTIDES
; TITLE OF INVENTION: FOR KIDNEY EPITHELIAL CELLS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRINKS, HOPER, GILSON & LIONE
; STREET: NBC Tower - Suite 3600, 455 N. Cityfront
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60611-5599
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,775
; FILING DATE: 20-NOV-1997
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin, Alice O.
; REGISTRATION NUMBER: 35,601
; REFERENCE/DOCKET NUMBER: 7814/27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-321-4200
; TELEFAX: 312-321-4299
; INFORMATION FOR SEQ ID NO: 48:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-775-48

Query Match 50.0%; Score 21; DB 3; Length 7;
Best Local Similarity 75.0%; Pred. NO. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGHL 5
DB 3 VGHL 6

RESULT 6
; US-08-530-342A-15
; Sequence 15, Application US/08530342A
; Patent No. 6143275
; GENERAL INFORMATION:
; APPLICANT: HILGER, CHRISTOPH-STEPH
; APPLICANT: DINKELBORG, LUDGER
; APPLICANT: KRAMP, WOLFGANG
; APPLICANT: SCHIER, HANS-MARTIN
; TITLE OF INVENTION: TYPE S3N2 CHELATORS FOR RADIO
; TITLE OF INVENTION: ACTIVE ISOTOPES, THEIR METAL COMPLEXES AND
; TITLE OF INVENTION: THEIR DIAGNOSTIC AND THERAPEUTICAL USE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOOD, PHILLIPS, VAN SANTEN, CLARK &
; STREET: 500 West Madison Street, Suite 3800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60661-2511
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: COMPAQ ProLinea 4/25s
; OPERATING SYSTEM: DOS

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; SOFTWARE: WordPerfect for Windows 6.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,342A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DE94/00370
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: P 43 11 022.3
; FILING DATE: 31-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mortimer, John S.
; REGISTRATION NUMBER: 30,407
; REFERENCE/DOCKET NUMBER: 1214.00008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/876-1800
; TELEFAX: 312/876-2020
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-530-342A-15

Query Match 50.0%; Score 21; DB 4; Length 7;
Best Local Similarity 66.7%; Pred. NO. 1.9e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GHYIL 8
DB 1 GHLDII 6

RESULT 7
; US-09-473-355-1
; Sequence 1, Application US/09473355
; Patent No. 6262027
; GENERAL INFORMATION:
; APPLICANT: Kudsk, Kenneth A.
; TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal
; FILE REFERENCE: 44137-5001-02-US
; CURRENT APPLICATION NUMBER: US/09/473,355
; CURRENT FILING DATE: 1999-12-28
; EARLIER APPLICATION NUMBER: US 09/067,032
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: US 08/842,877
; EARLIER FILING DATE: 1997-04-17
; EARLIER APPLICATION NUMBER: US 60/029,689
; EARLIER FILING DATE: 1996-10-31
; EARLIER APPLICATION NUMBER: US 60/015,835
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Bombina bombina
; US-09-473-355-1

Query Match 50.0%; Score 21; DB 4; Length 7;
Best Local Similarity 75.0%; Pred. NO. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGHL 5
DB 1

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DB	3	VGHL	6	0;
US-09-067-032-1	US-09-067-032-1	US-09-067-032-1	US-09-067-032-1	US-09-067-032-1
Sequence 1, Application US/09067032	Sequence 1, Application US/09067032	Sequence 1, Application US/09067032	Sequence 1, Application US/09067032	Sequence 1, Application US/09067032
Patent No. 6271202	Patent No. 6271202	Patent No. 6271202	Patent No. 6271202	Patent No. 6271202
GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:	GENERAL INFORMATION:
APPLICANT: Kugsek, Kenneth A.	APPLICANT: Kugsek, Kenneth A.	APPLICANT: Kugsek, Kenneth A.	APPLICANT: Kugsek, Kenneth A.	APPLICANT: Kugsek, Kenneth A.
TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal	TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal	TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal	TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal	TITLE OF INVENTION: Reduction of Impairment of Respiratory Tract Mucosal
FILE REFERENCE: 44137-5001-01-US	FILE REFERENCE: 44137-5001-01-US	FILE REFERENCE: 44137-5001-01-US	FILE REFERENCE: 44137-5001-01-US	FILE REFERENCE: 44137-5001-01-US
CURRENT APPLICATION NUMBER: US/09/067,032	CURRENT APPLICATION NUMBER: US/09/067,032	CURRENT APPLICATION NUMBER: US/09/067,032	CURRENT APPLICATION NUMBER: US/09/067,032	CURRENT APPLICATION NUMBER: US/09/067,032
EARLIER FILING DATE: 1998-04-28	EARLIER FILING DATE: 1998-04-28	EARLIER FILING DATE: 1998-04-28	EARLIER FILING DATE: 1998-04-28	EARLIER FILING DATE: 1998-04-28
EARLIER FILING DATE: 1997-04-17	EARLIER FILING DATE: 1997-04-17	EARLIER FILING DATE: 1997-04-17	EARLIER FILING DATE: 1997-04-17	EARLIER FILING DATE: 1997-04-17
EARLIER FILING DATE: 1996-10-31	EARLIER FILING DATE: 1996-10-31	EARLIER FILING DATE: 1996-10-31	EARLIER FILING DATE: 1996-10-31	EARLIER FILING DATE: 1996-10-31
EARLIER FILING DATE: 1996-04-19	EARLIER FILING DATE: 1996-04-19	EARLIER FILING DATE: 1996-04-19	EARLIER FILING DATE: 1996-04-19	EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 1	NUMBER OF SEQ ID NOS: 1	NUMBER OF SEQ ID NOS: 1	NUMBER OF SEQ ID NOS: 1	NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1	SOFTWARE: PatentIn Ver. 2.1	SOFTWARE: PatentIn Ver. 2.1	SOFTWARE: PatentIn Ver. 2.1	SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1	SEQ ID NO 1	SEQ ID NO 1	SEQ ID NO 1	SEQ ID NO 1
LENGTH: 7	LENGTH: 7	LENGTH: 7	LENGTH: 7	LENGTH: 7
TYPE: PRT	TYPE: PRT	TYPE: PRT	TYPE: PRT	TYPE: PRT
ORGANISM: Homo sapiens	ORGANISM: Homo sapiens	ORGANISM: Homo sapiens	ORGANISM: Homo sapiens	ORGANISM: Homo sapiens
US-09-067-032-1	US-09-067-032-1	US-09-067-032-1	US-09-067-032-1	US-09-067-032-1
Query Match	Query Match	Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity	Best Local Similarity	Best Local Similarity
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 IGHL 5	QY 2 IGHL 5	QY 2 IGHL 5	QY 2 IGHL 5	QY 2 IGHL 5
DB 3 VGHL 6	DB 3 VGHL 6	DB 3 VGHL 6	DB 3 VGHL 6	DB 3 VGHL 6
RESULT 9	RESULT 9	RESULT 9	RESULT 9	RESULT 9
5217955-30	5217955-30	5217955-30	5217955-30	5217955-30
Patent No. 5217955	Patent No. 5217955	Patent No. 5217955	Patent No. 5217955	Patent No. 5217955
APPLICANT: ABOGDEM, ARTHUR E.; NOREAU, JACQUES-PIERRE	APPLICANT: ABOGDEM, ARTHUR E.; NOREAU, JACQUES-PIERRE	APPLICANT: ABOGDEM, ARTHUR E.; NOREAU, JACQUES-PIERRE	APPLICANT: ABOGDEM, ARTHUR E.; NOREAU, JACQUES-PIERRE	APPLICANT: ABOGDEM, ARTHUR E.; NOREAU, JACQUES-PIERRE
TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG	TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG	TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG	TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG	TITLE OF INVENTION: TREATMENT OF CANCER WITH PEPTIDE ANALOG
OF BOMBESIN, GRP, LITOKIN OR NEURONEDIN	OF BOMBESIN, GRP, LITOKIN OR NEURONEDIN	OF BOMBESIN, GRP, LITOKIN OR NEURONEDIN	OF BOMBESIN, GRP, LITOKIN OR NEURONEDIN	OF BOMBESIN, GRP, LITOKIN OR NEURONEDIN
NUMBER OF SEQUENCES: 42	NUMBER OF SEQUENCES: 42	NUMBER OF SEQUENCES: 42	NUMBER OF SEQUENCES: 42	NUMBER OF SEQUENCES: 42
CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:	CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,225	APPLICATION NUMBER: US/08/520,225	APPLICATION NUMBER: US/08/520,225	APPLICATION NUMBER: US/08/520,225	APPLICATION NUMBER: US/08/520,225
FILING DATE: 05-MAY-1990	FILING DATE: 05-MAY-1990	FILING DATE: 05-MAY-1990	FILING DATE: 05-MAY-1990	FILING DATE: 05-MAY-1990
PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:	PRIOR APPLICATION DATA:
APPLICATION NUMBER: 440,039	APPLICATION NUMBER: 440,039	APPLICATION NUMBER: 440,039	APPLICATION NUMBER: 440,039	APPLICATION NUMBER: 440,039
FILING DATE: 21-NOV-1989	FILING DATE: 21-NOV-1989	FILING DATE: 21-NOV-1989	FILING DATE: 21-NOV-1989	FILING DATE: 21-NOV-1989
APPLICATION NUMBER: 408,125	APPLICATION NUMBER: 408,125	APPLICATION NUMBER: 408,125	APPLICATION NUMBER: 408,125	APPLICATION NUMBER: 408,125
FILING DATE: 15-SEP-1989	FILING DATE: 15-SEP-1989	FILING DATE: 15-SEP-1989	FILING DATE: 15-SEP-1989	FILING DATE: 15-SEP-1989
SEQ ID NO:30;	SEQ ID NO:30;	SEQ ID NO:30;	SEQ ID NO:30;	SEQ ID NO:30;
LENGTH: 7	LENGTH: 7	LENGTH: 7	LENGTH: 7	LENGTH: 7
5217955-30	5217955-30	5217955-30	5217955-30	5217955-30
Query Match	Query Match	Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity	Best Local Similarity	Best Local Similarity
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 IGHL 5	QY 2 IGHL 5	QY 2 IGHL 5	QY 2 IGHL 5	QY 2 IGHL 5
DB 3 VGHL 6	DB 3 VGHL 6	DB 3 VGHL 6	DB 3 VGHL 6	

Query Match 50.0%; Score 21; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 2 IGHL 5
 :|||
 DB 5 VGHL 8

RESULT 12
 US-08-168-390-13
 ; Sequence 13, Application US/08168390
 ; Patent No. 5620955
 ; GENERAL INFORMATION:
 ; APPLICANT: Knight, Martha
 ; APPLICANT: Takahashi, Kazuyuki
 ; APPLICANT: Chandrasekhar, Bhaskar
 ; TITLE OF INVENTION: Bombesin/Gastrin Releasing Peptide Antagonists
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/168,390
 ; FILING DATE: Herewich
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Goldstein, Jorge A.
 ; REGISTRATION NUMBER: 29,021
 ; REFERENCE/DOCKET NUMBER: 0871.0040001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 371-2600
 ; TELEFAX: (202) 371-2540
 ; TELEX: 248636 SSK
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 1
 ; OTHER INFORMATION: /note= "The amino-terminal residue
 ; OTHER INFORMATION: comprises one of several chemical end caps."
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 8
 ; OTHER INFORMATION: /note= "The carboxy-terminal
 ; OTHER INFORMATION: residue comprises an ethyl ester."
 ; US-08-168-390-13

Query Match 50.0%; Score 21; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 2 IGHL 5
 :|||
 DB 5 VGHL 8

RESULT 13
 US-08-387-634-3
 ; Sequence 3, Application US/08387634
 ; Patent No. 5767236

; GENERAL INFORMATION:
 ; APPLICANT: Kim, Sun Hyuk
 ; APPLICANT: Moreau, Jacques-Pierre
 ; TITLE OF INVENTION: LINEAR THERAPEUTIC PEPTIDES
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 ; COMPUTER: IBM PS/2 Model 502 or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/387,634
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/929,306A
 ; FILING DATE: 08/13/92
 ; APPLICATION NUMBER: US/07/520,226
 ; FILING DATE: 05/09/90

ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul I. and Tsao, Y. Rocky
 ; REGISTRATION NUMBER: 30,162 and 34,053
 ; REFERENCE/DOCKET NUMBER: 00537/040002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8
 ; TYPE: amino acid
 ; STRANDEDNESS: N/A
 ; TOPOLOGY: N/A
 ; FEATURE:
 ; OTHER INFORMATION:
 ; OTHER INFORMATION: The sequence contains at position 1 an acetylated His, rat
 ; OTHER INFORMATION: than a His, and has an amide C-terminus (i.e., COOH).
 ; US-08-387-634-3

Query Match 50.0%; Score 21; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.9e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGHL 5
 :|||
 DB 4 VGHL 7

RESULT 14
 US-08-337-127-9
 ; Sequence 9, Application US/08337127
 ; Patent No. 5871277
 ; GENERAL INFORMATION:
 ; APPLICANT: Coy, David H.
 ; APPLICANT: Moreau, Jacques-Pierre
 ; APPLICANT: Kim, Sun H.
 ; TITLE OF INVENTION: OCTAPEPTIDE BOMBESIN
 ; TITLE OF INVENTION: ANALOG
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,127
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/779,039
FILING DATE: 10/18/91
APPLICATION NUMBER: 07/502,438
FILING DATE: 03/30/90
APPLICATION NUMBER: 07/397,169
FILING DATE: 08/21/88
APPLICATION NUMBER: 07/376,555
FILING DATE: 07/07/89
APPLICATION NUMBER: 07/317,941
FILING DATE: 03/02/89
APPLICATION NUMBER: 07/282,328
FILING DATE: 12/09/88
APPLICATION NUMBER: 07/257,998
FILING DATE: 10/14/88
APPLICATION NUMBER: 07/248,771
FILING DATE: 09/23/88
APPLICATION NUMBER: 07/207,759
FILING DATE: 06/16/88
APPLICATION NUMBER: 07/204,171
FILING DATE: 06/08/88
APPLICATION NUMBER: 07/173,311
FILING DATE: 03/25/88
APPLICATION NUMBER: 07/100,571
FILING DATE: 09/24/87
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00537/009000D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The sequence contains at
OTHER INFORMATION: position 1 a pyroglutamate, rather than a glutamate,
OTHER INFORMATION: and has an methyl ester C-terminus (i.e., COOCH3),
OTHER INFORMATION: rather than a carboxyl C-terminus (i.e., COOH).

US-08-337-127-9

Query Match 50.0%; Score 21; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IGHLL 5
DB 5 VGHLL 8

RESULT 15
US-08-444-818-258
Sequence 258, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Ruetter, William J.
TITLE OF INVENTION: NERVE Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777

CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110,002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-444-818-258
Query Match 50.0%; Score 21; DB 4; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.9e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IGHLYIL 8
DB 2 VGGVYLL 8

Search completed: December 19, 2002, 16:58:35
Job time : 29 secs